

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 15:52:12 ; Search time 2574 Seconds
(without alignments)
9412.435 Million cell updates/sec

Title: US-10-043-160-5_COPY_1_500
Perfect score: 500
Sequence: 1 atatagagtaaaacttggtc.....cagaagtaagtggccgcag 500

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	500	100.0	7941	12	Li9899 Cloning vec
2	500	100.0	43228	6	A95274 Sequence 5
3	462	92.4	1086	6	AX212292 Sequence
4	462	92.4	1103	1	AF427127 Escherich
5	462	92.4	1106	6	I02541 Sequence 1
6	462	92.4	1652	6	I01971 Sequence 2
7	462	92.4	1905	6	AR027070 Sequence
8	462	92.4	1905	6	I86203 Sequence 9
9	462	92.4	2320	6	AR371194 Sequence
10	462	92.4	2320	6	BD008862 Hepatitis
11	462	92.4	2408	12	ASTNNAX9
12	462	92.4	2783	12	CVU47670
13	462	92.4	2846	12	SYNNOMPA
14	462	92.4	2870	6	AX107930
15	462	92.4	2913	12	CVU47322
16	462	92.4	3003	6	AR362785
17	462	92.4	3097	6	AX107931
18	462	92.4	3122	6	AR161211
19	462	92.4	3122	6	AR370166

20	462	92.4	3122	6	BD096800
21	462	92.4	3159	6	AX082146
22	462	92.4	3159	6	AX088825
23	462	92.4	3159	6	AX365120
24	462	92.4	3189	6	AX30504
25	462	92.4	3259	12	XXU16281
26	462	92.4	3273	12	AREF327
27	462	92.4	3274	12	SYNPR327V
28	462	92.4	3277	6	A30505
29	462	92.4	3277	6	A30507
30	462	92.4	3384	6	A30503
31	462	92.4	3387	6	E00974
32	462	92.4	3396	12	ASRSG424
33	462	92.4	3418	6	AR072541
34	462	92.4	3427	6	A30513
35	462	92.4	3427	6	A30515
36	462	92.4	3431	12	AF308739
37	462	92.4	3432	12	AF308741
38	462	92.4	3433	12	AF308740
39	462	92.4	3468	6	E00954
40	462	92.4	3473	6	AX766168
41	462	92.4	3473	6	AX815026
42	462	92.4	3477	6	E00952
43	462	92.4	3507	12	SYNPD8LUS
44	462	92.4	3516	6	AR202883
45	462	92.4	3541	6	E00953

ALIGNMENTS

RESULT 1
SYNCPVPTCF
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
ORIGIN
Query Match
Best Local Similarity
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATATATGAGTAAACTTGGTCTGACAGTACCAATGCTTAATCAGTACGAGGACCTATCTCA 60
DB 1530 ATATATGAGTAAACTTGGTCTGACAGTACCAATGCTTAATCAGTACGAGGACCTATCTCA 1599

SYNCPVPTCF 7941 bp DNA linear SYN 20-OCT-1999
Cloning vector cosmid pTCF DNA sequence encoding beta-lactamase gene.

Li9899
L19899.1 GI:310738
beta-lactamase.
Cloning vector pTCF
Cloning vector pTCF
other sequences; artificial sequences; vectors.

1 (bases 1 to 7941)
Pan.H.Q., Wang.Y.P., Chissos.S.L., Bodenteich.A., Wang.Z., Iyer,K., Clifton.S.W., Crabtree,J.S. and Roeb.B.A.

The complete nucleotide sequences of the SacBII Kan domain of the

PI pAD10-SacBII cloning vector and three cosmid cloning vectors:

PTCF, SYNPR, and LARIS116

Genet. Anal. Tech. Appl. 11 (5-6), 181-186 (1994)

95220138

7710784

a cosmid cloning vector constructed by F. Grosveld, Department of

Cell Biology, Erasmus University, Rotterdam, The Netherlands.

Location/Qualifiers

1..7941

/organism="Cloning vector pTCF"

/mol_type="genomic DNA"

/db_xref="taxon:106076"

1559..2419

/pseudo

/codon_start=1

/transl_table=11

/product="beta-lactamase"

Query Match 100.0%; Score 500; DB 12; Length 7941;

Best Local Similarity 100.0%; Pred. No. 1.4e-146; Indels 0; Gaps 0;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1530 ATATATGAGTAAACTTGGTCTGACAGTACCAATGCTTAATCAGTACGAGGACCTATCTCA 1599


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QY 301 AAGTAGTCCGCGAGTTAATAGTTGGCGCAAGTTGTTGCCATTGCTCGCAGGCATCGTGGT 360
DB 299 AAGTAGTCCGCGAGTTAATAGTTGGCGCAAGTTGTTGCCATTGCTCGCAGGCATCGTGGT 358
QY 361 GTACAGCTCGTGGTTCGTTGCTTCCATTCAGCTCCGCTTCCCAAGCATCAAGGCGAGT 420
DB 359 GTACAGCTCGTGGTTCGTTGCTTCCATTCAGCTCCGCTTCCCAAGCATCAAGGCGAGT 418
QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGT 480
DB 419 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGT 478
QY 481 CAGAGTAAGTTGGCCCGCAG 500
DB 479 CAGAGTAAGTTGGCCCGCAG 498

RESULT 4
AF427127/c
LOCUS 1103 bp DNA linear BCT 08-NOV-2001
DEFINITION Escherichia coli inhibitor-resistant beta-lactamase TEM-81
ACCESSION AF427127
VERSION AF427127.1 GI:16798369
KEYWORDS
SOURCE
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1 (bases 1 to 1103)
AUTHORS Leflon-Guibout,V., Speldooren,V., Heym,B. and Nicolas-Chanoine,M.
TITLE Epidemiological survey of amoxicillin-clavulanate resistance and
corresponding molecular mechanisms in Escherichia coli isolates in
France: new genetic features of bla(TEM) genes
JOURNAL Antimicrob. Agents Chemother. 44 (10), 2709-2714 (2000)
MEDLINE 2048741
PUBMED 10991849
REFERENCE 2 (bases 1 to 1103)
AUTHORS Leflon-Guibout,V., Speldooren,V., Heym,B. and
Nicolas-Chanoine,M.-H.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2001) Microbiology Service, Ambroise Pare
University Hospital, 9 avenue Charles de Gaulle, Boulogne 92100,
France

FEATURES
source Location/Qualifiers
1. .1103
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
209..1069
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/codon_start=1
/transl_table=11
/product="inhibitor-resistant beta-lactamase TEM-81"
/protein_id="AAL29433.1"
/db_xref="GI:16798370"
/translation="MSIQHPRVALIIPFFAFCPLPFAHPETLVKVAEDOLGARVGY
IEDLNSGKILESFRPEERFPMLSFTKVLCCGAVLSRVDAGQQLGRRIRHNSQNDLVE
YSPVTEKHGDTLSDSAAVTMSDNTAANLLTITGGPKELTAFLHNMGDHVRFL
DRWPELNEAIPNDRDTPMAAMATTLRLKLTLLASRQQLIDWMEADKVAQPL
LRSLAPAGNFIADKSGAGERSGIIAALGPDPGKPSRIVVIYTTGSAQTWDERNRQIA
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ORIGIN
Query Match 92.4%; Score 462; DB 1; Length 1103;
Best Local Similarity 99.2%; Pred. No. 1.2e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

1
QY 1 ATATATGAGTAAGTTCGCTGACAGTTACCAATGCTTAATCAGTAGGACCCTATCTCA 60
DB 1095 ATATATGAGTAAGTTCGCTGACAGTTACCAATGCTTAATCAGTAGGACCCTATCTCA 1036

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QY 61 GCGATCTGTCTATTTCGTTTCATCCCATAGTTGCTGCAACTCCCGTCGTGTAGATAACT 120
DB 1035 GCGATCTGTCTATTTCGTTTCAT--CATAGTTGCTG--ACTCCCGTCGTGTAGATAACT 979
QY 121 ACCATACGGGAGGGCTTACCATCTGCGCCCGAGTCTGCAATGATACCGCGAAGACCCACG 180
DB 978 ACCATACGGGAGGGCTTACCATCTGCGCCCGAGTCTGCAATGATACCGCG--AGACCCACG 920
QY 181 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCCGCGAAGGCCGAGCAGAG 240
DB 919 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCCGCGAAGGCCGAGCAGAG 860
QY 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTTAATTGTTGCGGGAAGCTAGAGT 300
DB 859 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTTAATTGTTGCGGGAAGCTAGAGT 800
QY 301 AAGTAGTTCGCGAGTTAATAGTTTGGCGCAAGTTGTTGCCATTGCTCGCAGGCATCGTGGT 360
DB 799 AAGTAGTTCGCGAGTTAATAGTTTGGCGCAAGTTGTTGCCATTGCTCGCAGGCATCGTGGT 740
QY 361 GTCACGCTCGTGGTTCGTTGCTTTCATTCAGCTCCGCTTCCCAAGCATCAAGGCGAGT 420
DB 739 GTCACGCTCGTGGTTCGTTGCTTTCATTCAGCTCCGCTTCCCAAGCATCAAGGCGAGT 680
QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGT 480
DB 679 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGT 620
QY 481 CAGAGTAAGTTGGCCCGCAG 500
DB 619 CAGAGTAAGTTGGCCCGCAG 600

RESULT 5
102541/c
LOCUS 1106 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4565785.
ACCESSION 102541
VERSION 102541.1 GI:268188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1106)
AUTHORS Gilbert,W., Broome,S.A., Villa-Komaroff,L.J. and Efstratiadis,A.A.
TITLE Recombinant DNA molecule
JOURNAL Patent: US 4565785-A 1 21-JAN-1986;
The President and Fellows of Harvard College; Cambridge, MA
FEATURES
source Location/Qualifiers
1. .1106
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 92.4%; Score 462; DB 6; Length 1106;
Best Local Similarity 99.2%; Pred. No. 1.2e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

1
QY 1 ATATATGAGTAAGTTCGCTGACAGTTACCAATGCTTAATCAGTAGGACCCTATCTCA 60
DB 1098 ATATATGAGTAAGTTCGCTGACAGTTACCAATGCTTAATCAGTAGGACCCTATCTCA 1039
QY 61 GCGATCTGTCTATTTCGTTTCATCCCATAGTTGCTGCAACTCCCGTCGTGTAGATAACT 120
DB 1038 GCGATCTGTCTATTTCGTTTCAT--CATAGTTGCTG--ACTCCCGTCGTGTAGATAACT 982
QY 121 ACCATACGGGAGGGCTTACCATCTGCGCCCGAGTCTGCAATGATACCGCGAAGACCCACG 180
DB 981 ACCATACGGGAGGGCTTACCATCTGCGCCCGAGTCTGCAATGATACCGCG--AGACCCACG 923
QY 181 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCCGCGAAGGCCGAGCAGAG 240

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Db      922  CTCACGGCTCCAGATTATACAGATAAACCAGCCAGCCGGAAGGCGCGCAGAG 863
Qy      241  TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 300
Db      862  TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 803
Qy      301  AAGTAGTTCGCCAGTTAAATAGTTTGGCAACGTTGTCGATGTCGAGGCGATCGTGT 360
Db      802  AAGTAGTTCGCCAGTTAAATAGTTTGGCAACGTTGTCGATGTCGAGGCGATCGTGT 743
Qy      361  GTACCGCTCGTCTGTTGATGCTTCATTACGCTCGGTTCCTCAACGATCAAGCGAGT 420
Db      742  GTACCGCTCGTCTGTTGATGCTTCATTACGCTCGGTTCCTCAACGATCAAGCGAGT 683
Qy      421  TACATGATCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGGTCTCCGATCGTTGT 480
Db      682  TACATGATCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGGTCTCCGATCGTTGT 623
Qy      481  CAGAAGTAAGTTGGCCGCGAG 500
Db      622  CAGAAGTAAGTTGGCCGCGAG 603

RESULT 6
LOCUS      I01971      1652 bp ss-DNA      linear      PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4795699.
ACCESSION  I01971
VERSION     I01971.1  GI:269733
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1652)
AUTHORS     Tabor,S. and Richardson,C.C.
TITLE       T7 DNA polymerase
JOURNAL     Patent: US 4795699-A 2 03-JAN-1989;
FEATURES    Location/Qualifiers
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              /mol_type="unassigned DNA"

ORIGIN
Query Match      92.4%; Score 462; DB 6; Length 1652;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

Qy      1  ATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
Db      558  ATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 617
Qy      61  GCGATCTGCTATTTCGTTATCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT 120
Db      618  GCGATCTGCTATTTCGTTATCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT 674
Qy      121  ACGATACGGGAGGCTTACCATCTGCCCCAGTCTGCAATGATACCGCAAGACCCACG 180
Db      675  ACGATACGGGAGGCTTACCATCTGCCCCAGTCTGCAATGATACCGCAAGACCCACG 733
Qy      181  CTCACCGGCTCCAGATTATACAGCAATAAACAGCCAGCCGGAAGGCGCGCAGAAG 240
Db      734  CTCACCGGCTCCAGATTATACAGCAATAAACAGCCAGCCGGAAGGCGCGCAGAAG 793
Qy      241  TGGTCTCGCAACTTTATCCGCTCCATCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 300
Db      794  TGGTCTCGCAACTTTATCCGCTCCATCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 853
Qy      301  AAGTAGTTCGCCAGTTAAATAGTTTGGCAACGTTGTCGATGTCGAGGCGATCGTGT 360
Db      854  AAGTAGTTCGCCAGTTAAATAGTTTGGCAACGTTGTCGATGTCGAGGCGATCGTGT 913
Qy      361  GTACCGCTCGTCTGTTGATGCTTCATTACGCTCGGTTCCTCAACGATCAAGCGAGT 420
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Db      914  GTACCGCTCGTCTGTTGATGCTTCATTACGCTCCGTTCCCAAGGATCAAGCGGAGT 973
Qy      421  TACATGATCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGGTCTCCGATCGTTGT 480
Db      974  TACATGATCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGGTCTCCGATCGTTGT 1033
Qy      481  CAGAAGTAAGTTGGCCGCGAG 500
Db      1034  CAGAAGTAAGTTGGCCGCGAG 1053

RESULT 7
LOCUS      AR027070      1905 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5856142.
ACCESSION  AR027070
VERSION     AR027070.1  GI:5937910
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1905)
AUTHORS     Legoux,R., Maldonado,P. and Salome,M.
TITLE       Method for the extraction of periplasmic proteins from prokaryotic
            microorganisms in the presence of arginine
JOURNAL     Patent: US 5856142-A 9 05-JAN-1999;
FEATURES    Location/Qualifiers
            source
              1..1905
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      92.4%; Score 462; DB 6; Length 1905;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

Qy      1  ATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
Db      817  ATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 876
Qy      61  GCGATCTGCTATTTCGTTATCCATGCTCCCTGCAACTCCCGCTCGTGTAGATAACT 120
Db      877  GCGATCTGCTATTTCGTTATCCATGCTCCCTGCAACTCCCGCTCGTGTAGATAACT 933
Qy      121  ACGATACGGGAGGCTTACCATCTGCCCCAGTCTGCAATGATACCGCAAGACCCACG 180
Db      934  ACGATACGGGAGGCTTACCATCTGCCCCAGTCTGCAATGATACCGCAAGACCCACG 992
Qy      181  CTCACCGGCTCCAGATTATACAGCAATAAACAGCCAGCCGGAAGGCGCGCAGAAG 240
Db      993  CTCACCGGCTCCAGATTATACAGCAATAAACAGCCAGCCGGAAGGCGCGCAGAAG 1052
Qy      241  TGGTCTCGCAACTTTATCCGCTCCATCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 300
Db      1053  TGGTCTCGCAACTTTATCCGCTCCATCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 1112
Qy      301  AAGTAGTTCGCCAGTTAAATAGTTTGGCAACGTTGTCGATGTCGAGGCGATCGTGT 360
Db      1113  AAGTAGTTCGCCAGTTAAATAGTTTGGCAACGTTGTCGATGTCGAGGCGATCGTGT 1172
Qy      361  GTACCGCTCGTCTGTTGATGCTTCATTACGCTCCGTTCCCAACGATCAAGCGGAGT 420
Db      1173  GTACCGCTCGTCTGTTGATGCTTCATTACGCTCCGTTCCCAACGATCAAGCGGAGT 1232
Qy      421  TACATGATCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGGTCTCCGATCGTTGT 480
Db      1233  TACATGATCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGGTCTCCGATCGTTGT 1292
Qy      481  CAGAAGTAAGTTGGCCGCGAG 500
Db      1293  CAGAAGTAAGTTGGCCGCGAG 1312
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RESULT 8
186203 LOCUS
DEFINITION Sequence 9 from patent US 5700665.
ACCESSION 186203
VERSION 186203.1 GI:3205921
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1905)
AUTHORS Legoux,R., Maldonado,P. and Salome,M.
TITLE Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: US 5700665-A 9 23-DEC-1997;
FEATURES
source 1..1905
/organism="unknown"
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ORIGIN
Query Match 92.4%; Score 462; DB 6; Length 1905;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
Qy 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCA 60
Db 817 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCA 876
Qy 61 GCGATCTGTCTATTTCGTTTCATCCATAGTTGCTGCAATCTCCCGTCTGTGTAGATAACT 120
Db 877 GCGATCTGTCTATTTCGTTTCAT -CCATAGTTGCTG -ACTCCCGTCTGTGTAGATAACT 933
Qy 121 ACATAGCGGAGGGCTTACCATCTGCGCCAGTCTGCAATGATACCGCGAAGCCACG 180
Db 934 ACATAGCGGAGGGCTTACCATCTGCGCCAGTCTGCAATGATACCGCG -AGACCCACG 992
Qy 181 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCGGAGGCGGAGGCGCAGAAG 240
Db 993 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCGGAGGCGGAGGCGCAGAAG 1052
Qy 241 TGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 300
Db 1053 TGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 1112
Qy 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCGCAATGATACCGCGAAGCCACG 360
Db 1113 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCGCAATGATACCGCG -AGACCCACG 1172
Qy 361 GTCACGCTCGTCTGTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT 420
Db 1173 GTCACGCTCGTCTGTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT 1232
Qy 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCTCGGTCCTCCGATCGTTGT 480
Db 1233 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCTCGGTCCTCCGATCGTTGT 1292
Qy 481 CAGAGTAAGTTGGCCGCGAG 500
Db 1293 CAGAGTAAGTTGGCCGCGAG 1312

RESULT 9
AR371194/c LOCUS
DEFINITION Sequence 13 from patent US 6395471.
ACCESSION AR371194
VERSION AR371194.1 GI:34608123
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 2320)
AUTHORS Jang,S.K. and Hahn,B.
TITLE Hepatitis C surrogate virus for testing the activity of hepatitis C
virus protease, a recombinant gene and a use thereof
JOURNAL Patent: US 6395471-A 13 28-MAY-2002;
FEATURES
source 1..2320
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 92.4%; Score 462; DB 6; Length 2320;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
Qy 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCA 60
Db 2277 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCA 2218
Qy 61 GCGATCTGTCTATTTCGTTTCATCCATAGTTGCTGCAATCTCCCGTCTGTGTAGATAACT 120
Db 2217 GCGATCTGTCTATTTCGTTTCAT -CCATAGTTGCTG -ACTCCCGTCTGTGTAGATAACT 2161
Qy 121 ACATAGCGGAGGGCTTACCATCTGCGCCAGTCTGCAATGATACCGCGAAGCCACG 180
Db 2160 ACATAGCGGAGGGCTTACCATCTGCGCCAGTCTGCAATGATACCGCG -AGACCCACG 2102
Qy 181 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCGGAGGCGGAGGCGCAGAAG 240
Db 2101 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCGGAGGCGGAGGCGCAGAAG 2042
Qy 241 TGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 300
Db 2041 TGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 1982
Qy 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCGCAATGATACCGCGAAGCCACG 360
Db 1981 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCGCAATGATACCGCG -AGACCCACG 1922
Qy 361 GTCACGCTCGTCTGTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT 420
Db 1921 GTCACGCTCGTCTGTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT 1862
Qy 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCTCGGTCCTCCGATCGTTGT 480
Db 1861 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCTCGGTCCTCCGATCGTTGT 1802
Qy 481 CAGAGTAAGTTGGCCGCGAG 500
Db 1801 CAGAGTAAGTTGGCCGCGAG 1782

RESULT 10
BD008862/c LOCUS
DEFINITION
ACCESSION BD008862
VERSION BD008862.1 GI:18637235
KEYWORDS JP 2001503967-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 2320)
AUTHORS Jang,S.K. and Hahn,B.S.
TITLE Hepatitis C surrogate virus for testing the activity of hepatitis C
virus protease, a recombinant gene and a use thereof
JOURNAL Patent: JP 2001503967-A 4 27-MAR-2001;
LG CHEMICALS CO LTD, OHANG UNIVERSITY OF SCIENCE AND TECHNOLOGY
FOUNDATION
OS Artificial Sequence

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PN JP 2001503967-A/4
PD 27-MAR-2001
PF 25-JUN-1997 JP 1998504001
PR 28-JUN-1996 KR 1996/24910
PI SUNG KEY JANG, BUM SUK HAHM
PC C12N15/51,C12Q1/70
CC
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FT

Key Location/Qualifiers
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FEATURES
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1. .2320
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ORIGIN
Query Match 92.4%; Score 462; DB 6; Length 2320;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAAGTGGAGGACCTATCTCA 60
DB 2277 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAAGTGGAGGACCTATCTCA 2218
QY 61 GCGATCTGCTTATTTGCTTATCCATAGTTCCTGCACTCCCGTCCGTTGAGATAACT 120
DB 2217 GCGATCTGCTTATTTGCTTATCCATAGTTCCTGCACTCCCGTCCGTTGAGATAACT 2161
QY 121 ACGATACGGAGGGCTTACCATCTGGCCCGAGTCTGCAATGATACCGGAGACCCACG 180
DB 2160 ACGATACGGAGGGCTTACCATCTGGCCCGAGTCTGCAATGATACCGGAGACCCACG 2102
QY 181 CTCACCGGCTCCAGATTATCAGCAATPAAACCGACCGAGCGGAGGCGGAGGAG 240
DB 2101 CTCACCGGCTCCAGATTATCAGCAATPAAACCGACCGAGCGGAGGCGGAGGAG 2042
QY 241 TGGTCTGCACTTATTCGCGCTCCATCCAGTCTTATTAATTTGTCGCGGAGGAGTAGGT 300
DB 2041 TGGTCTGCACTTATTCGCGCTCCATCCAGTCTTATTAATTTGTCGCGGAGGAGTAGGT 1982
QY 301 AAGTAGTTCGCGAGTAAATAGTTTGCACAAAGTTGTCGCAATGCTGCGGAGGAGTAGGT 360
DB 1981 AAGTAGTTCGCGAGTAAATAGTTTGCACAAAGTTGTCGCAATGCTGCGGAGGAGTAGGT 1922
QY 361 GTCACGCTGCTGTTGATAGTTCATTCAGTCCGGTTCCTCCAAAGGAGGAGT 420
DB 1921 GTCACGCTGCTGTTGATAGTTCATTCAGTCCGGTTCCTCCAAAGGAGGAGT 1862
QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTTCGCTCCGATCGTTGT 480
DB 1861 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTTCGCTCCGATCGTTGT 1802
QY 481 CAGAAGTAAGTTGGCGGAG 500
DB 1801 CAGAAGTAAGTTGGCGGAG 1782

RESULT 11
ASTNMAX9
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

ASTNMAX9
Artificial DNA for pTnMax9 mini-transposon.
Z50143
Z50143.1 GI:938044
beta-lactamase; chloramphenicol acetyltransferase; mini-transposon;
transposon.
synthetic construct
other sequences: artificial sequences.
1 (bases 1 to 2408)
Kahrs,A.F., Odenbret,S., Schmitt,W., Heuermann,D., Meyer,T.F. and
Haas,R.
An improved TnMax mini-transposon system suitable for sequencing,

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE

shuttle mutagenesis and gene fusions
Gene 167 (1-2), 53-57 (1995)
96144248
8566811
2 (bases 1 to 2408)
Haas,R.
Improved TnMax mini-transposon system suitable for sequencing,
shuttle mutagenesis and gene fusions
Gene
3 (bases 1 to 2408)
Haas,R.
Direct Submission
Submitted (19-JUL-1995) Rainer Haas, Infektionsbiologie,
Max-Planck-Institut fuer, Biologie, Spemannstr. 34, Tuebingen,
B.W., D-72076, Germany
Location/Qualifiers
1. .2408
/organism="synthetic construct"
/mol_type="other DNA"
/db_xref="taxon:32630"
/lab_host="Escherichia coli K12"
1. .2408
/transposon="pTnMax9"
/rpt_type=INVERTED
1. .41
complement (42. .59)
/note="M13-20 forward primer (M13-FP)"
complement (77. .263)
/note="fd-terminator (tfd)"
complement (264. .923)
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/transl_table=11
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/protein_id="CAA90506.1"
/db_xref="GI:938045"
/translation="MEKKITGTVTVDISQWHRKEHFEAFQSVACCTYNQTVOLDITAF
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ANMNDFFAPVFTMGKYTQGDVLMPLAIQVHHAVCDFHVGRLNELQQYCDWEQGG
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complement (924. .1026)
/gene="catGC"
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/gene="catGC"
/note="gonococcal opa promoter"
1027. .1260
/note="rep-origin of bacteriophage fd (orf1d)"
1261. .1428
/function="resolution site (res)"
complement (1554. .2342)
/product="mature beta-lactamase (Blam)"
2349. .2366
/note="M13 reverse primer (M13-RP1)"
2367. .2408
/rpt_type=INVERTED

gene
promoter
rep_origin
misc_feature
mat_peptide
primer_bind
repeat_region

Query Match 92.4%; Score 462; DB 12; Length 2408;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAAGTGGAGGACCTATCTCA 60
DB 1525 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAAGTGGAGGACCTATCTCA 1584
QY 61 GCGATCTGCTTATTTGCTTATCCATCTGCCCCAGTCTGCCAATGATACCCGTCGTAGATAACT 120
DB 1585 GCGATCTGCTTATTTGCTTATCCATCTGCCCCAGTCTGCCAATGATACCCGTCGTAGATAACT 1641
QY 121 ACGATACGGAGGGCTTACCATCTGGCCCGAGTCTGCAATGATACCGGAGACCCACG 180
DB 1642 ACGATACGGAGGGCTTACCATCTGGCCCGAGTCTGCAATGATACCGGAGACCCACG 1700

ORIGIN
Query Match 92.4%; Score 462; DB 12; Length 2408;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAAGTGGAGGACCTATCTCA 60
DB 1525 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAAGTGGAGGACCTATCTCA 1584
QY 61 GCGATCTGCTTATTTGCTTATCCATCTGCCCCAGTCTGCCAATGATACCCGTCGTAGATAACT 120
DB 1585 GCGATCTGCTTATTTGCTTATCCATCTGCCCCAGTCTGCCAATGATACCCGTCGTAGATAACT 1641
QY 121 ACGATACGGAGGGCTTACCATCTGGCCCGAGTCTGCCAATGATACCCGTCGTAGATAACT 180
DB 1642 ACGATACGGAGGGCTTACCATCTGGCCCGAGTCTGCCAATGATACCCGTCGTAGATAACT 1700


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QY 181 CTCACGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCCGAGCCGAGAAG 240
Db 1701 CTCACGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCCGAGCCGAGAAG 1760
QY 241 TGGTCTCTGCAACTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAGCTAGAGT 300
Db 1761 TGGTCTCTGCAACTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAGCTAGAGT 1820
QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCCAAAGCTTTGTTGCCATTGCTGCAGGCATCGTGGT 360
Db 1821 AAGTAGTTCGCCAGTTAATAGTTTGGCCAAAGCTTTGTTGCCATTGCTGCAGGCATCGTGGT 1880
QY 361 GTCACGCTCGCTGTTGGTAGTTCATTCAGCTCCGTTCCCAAGCATCAAGGCGAGT 420
Db 1881 GTCACGCTCGCTGTTGGTAGTTCATTCAGCTCCGTTCCCAAGCATCAAGGCGAGT 1940
QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGCTCCCGATCGTTGT 480
Db 1941 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGCTCCCGATCGTTGT 2000
QY 481 CAGAAGTAAAGTTGGCCGCGAG 500
Db 2001 CAGAAGTAAAGTTGGCCGCGAG 2020

RESULT 12
CVU47670
LOCUS
DEFINITION
Cloning vector pJDC406, 2783 bp DNA circular SYN 20-FEB-1996
coli, complete sequence.
U47670.1 GI:1197852
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Cloning vector pJDC406
Other sequences; artificial sequences; vectors.
REFERENCE
1 (bases 1 to 2783)
AUTHORS
Coleman,J., Green,P.J. and Inouye,M.
TITLE
The use of RNAs complementary to specific mRNAs to regulate the
expression of individual bacterial genes
JOURNAL
Cell 37 (2), 429-436 (1984)
MEDLINE
84205677
PUBMED
6202422
REFERENCE
2 (bases 1 to 2783)
AUTHORS
Coleman,J., Hirashima,A., Inokuchi,Y., Green,P.J. and Inouye,M.
TITLE
A novel immune system against bacteriophage infection using
complementary RNA (micRNA)
JOURNAL
Nature 315 (6020), 601-603 (1985)
MEDLINE
85240542
PUBMED
2409446
REFERENCE
3 (bases 1 to 2783)
AUTHORS
Coleman,J., Hirashima,A., Inokuchi,Y., Green,P.J. and Inouye,M.
TITLE
Direct Submission
Submitted (30-JAN-1996) Jack Coleman, Biochemistry and Molecular
Biology, Louisiana State University - Medical Center, 1901 Perdido
St., New Orleans, LA 70112, USA
FEATURES
source
1..2783
/organism="Cloning vector pJDC406"
/mol_type="genomic DNA"
/specific_host="Escherichia coli"
/db_xref="taxon:45852"
/notes="antisense RNA expression vector"
misc_feature
1..417
/notes="portable expression cassette on SmaI fragment; SmaI
expression cassette may be inserted in a second vector"
288..297
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or EcoRI sites"
complement(1717..2577)
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/transl_table=11
/product="beta-lactamase"
misc_feature
1
CDS

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DRREPELNEAIPIIDERDITPMAAMATTIRKLITGELLTLASRQQLIDWHEADKVAQPL
LKSALPAGFWFIADKSGAGERSGRIITALLGPDPKPSRI VVIYITGSAQTMDERNRQIA
EIGASLIKHW"
ORIGIN
Query Match 92.4%; Score 462; DB 12; Length 2783;
Best Local Similarity 99.2%; Pred. No. 1.3e-134; Indels 4; Gaps 3;
Matches 496; Conservative 0; Mismatches 0;
QY 1 ATATATGAGTAAACTTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACTATCTCA 60
Db 1691 ATATATGAGTAAACTTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACTATCTCA 1750
QY 61 GCGATCTGTCTATTTCGTTTCATCCCATAGTTGCTGCAACTCCCGTCTGTGTAGATAACT 120
Db 1751 GCGATCTGTCTATTTCGTTTCAT-CCATAGTTGCTG- -ACTCCCGTCTGTGTAGATAACT 1807
QY 121 ACGATACGGGAGGCTTACCATCTGSCCCAGTGTGCAATGATATCCGGAAGACCCACG 180
Db 1808 ACGATACGGGAGGCTTACCATCTGSCCCAGTGTGCAATGATATCCGGAAGACCCACG 1866
QY 181 CTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGCCGAGCCAGAAG 240
Db 1867 CTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGCCGAGCCAGAAG 1926
QY 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAGCTAGAGT 300
Db 1927 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAGCTAGAGT 1986
QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCCAAAGCTTTGTTGCCATTGCTGCAGGCATCGTGGT 360
Db 1987 AAGTAGTTCGCCAGTTAATAGTTTGGCCAAAGCTTTGTTGCCATTGCTGCAGGCATCGTGGT 2046
QY 361 GTCACGCTCGTCTGTTGGTAGTTCATTCAGCTCCGTTCCCAAGCATCAAGGCGAGT 420
Db 2047 GTCACGCTCGTCTGTTGGTAGTTCATTCAGCTCCGTTCCCAAGCATCAAGGCGAGT 2106
QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGCTCCCGATCGTTGT 480
Db 2107 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCGCTCCCGATCGTTGT 2166
QY 481 CAGAAGTAAAGTTGGCCGCGAG 500
Db 2167 CAGAAGTAAAGTTGGCCGCGAG 2186

RESULT 13
SYNOMPA/C
LOCUS
DEFINITION
Cloning vector DNA, clone pTO-N.
ACCESSION
M59367 M34008
VERSION
M59367.1 GI:208909
KEYWORDS
unidentified cloning vector
SOURCE
unidentified cloning vector
ORGANISM
other sequences; artificial sequences; vectors.
REFERENCE
1 (bases 1 to 2846)
AUTHORS
Deng,T.L., Noel,J.P. and Tsai,M.D.
TITLE
A novel expression vector for high-level synthesis and secretion of
foreign proteins in Escherichia coli: overproduction of bovine
pancreatic phospholipase A2
JOURNAL
Gene 93 (2), 229-234 (1990)
MEDLINE
91033032
PUBMED
2227436
COMMENT
Original source text: Cloning vector DNA, clone pTO-N.
FEATURES
Location/Qualifiers
1..2846
/organism="unidentified cloning vector"

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Query Match          92.4%; Score 462; DB 12; Length 2846;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

promoter
misc_feature
notes="OmpA signal"

ORIGIN
1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
1394 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 1335
61 GCGATCTGCTATTCGTTTCATCCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT 120
1334 GCGATCTGCTATTCGTTTCAT - CCAATGTTGCTG - - ACTCCCGCTCGTGTAGATAACT 1278
121 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAGAACCCACG 180
1277 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGG - AGACCCACG 1219
181 CTCACGGCTCCAGATTATCAGCAATAAACACGACCGCGGAGCGGCGAGGAG 240
1218 CTCACGGCTCCAGATTATCAGCAATAAACACGACCGCGGAGCGGAGCGGAGGAG 1159
241 TGGTCTGCAACTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 300
1158 TGGTCTGCAACTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 1099
301 AAGTAGTTCGCCAGTTAATAGTTGGCCAAAGTGTGGCAATGCTGCGAGGCATCGTGGT 360
1098 AAGTAGTTCGCCAGTTAATAGTTGGCCAAAGTGTGGCAATGCTGCGAGGCATCGTGGT 1039
361 GTCACGCTCGCTGTTGGTAGTTCATTCAGTCCGGTTCCTCCAGATCAAGGCGAGT 420
1038 GTCACGCTCGCTGTTGGTAGTTCATTCAGTCCGGTTCCTCCAGATCAAGGCGAGT 979
421 TACATGATCCCCATGTTGTGCAAAAAGCGGTTAGTCTCGTCCCTCCGATCGTTGT 480
978 TACATGATCCCCATGTTGTGCAAAAAGCGGTTAGTCTCGTCCCTCCGATCGTTGT 919
481 CAGAAAGTAAAGTTGCCCGAG 500
918 CAGAAAGTAAAGTTGCCCGAG 899

RESULT 14
AX107930
LOCUS          2870 bp      DNA      linear      PAT 30-APR-2001
DEFINITION    Sequence 58 from Patent WO0125466.
ACCESSION    AX107930
VERSION      AX107930.1 GI:13923313
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Slingsby,J., Kingman,S.M., Rohll,J.O. and Slade,A.O.
TITLE         Producer cell for the production of retroviral vectors
JOURNAL       Patent: WO 0125466-A 58 12-APR-2001;
              Oxford Biomedica (UK) Limited (GB)
FEATURES      Location/Qualifiers
source        1. .2870
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic sequence"

ORIGIN
1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
1490 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 1549
61 GCGATCTGCTATTCGTTTCATCCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT 120
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Query Match          92.4%; Score 462; DB 6; Length 2870;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
1607 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 1666
61 GCGATCTGCTATTCGTTTCATCCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT 120
1667 GCGATCTGCTATTCGTTTCAT - CCAATGTTGCTG - - ACTCCCGCTCGTGTAGATAACT 1723
121 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAGAACCCACG 180
1724 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGG - AGACCCACG 1782
181 CTCACGGCTCCAGATTATCAGCAATAAACACGACCGCGGAGCGGCGAGGAG 240
1783 CTCACGGCTCCAGATTATCAGCAATAAACACGACCGCGGAGCGGCGAGGAG 1842
241 TGGTCTGCAACTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 300
1843 TGGTCTGCAACTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 1902
301 AAGTAGTTCGCCAGTTAATAGTTTGGCCAAAGTGTGGCAATGCTGCGAGGCATCGTGGT 360
1903 AAGTAGTTCGCCAGTTAATAGTTTGGCCAAAGTGTGGCAATGCTGCGAGGCATCGTGGT 1962
361 GTCACGCTCGCTGTTGGTAGTTCATTCAGTCCGGTTCCTCCAGATCAAGGCGAGT 420
1963 GTCACGCTCGCTGTTGGTAGTTCATTCAGTCCGGTTCCTCCAGATCAAGGCGAGT 2022
421 TACATGATCCCCATGTTGTGCAAAAAGCGGTTAGTCTCGTCCCTCCGATCGTTGT 480
2023 TACATGATCCCCATGTTGTGCAAAAAGCGGTTAGTCTCGTCCCTCCGATCGTTGT 2082
481 CAGAAAGTAAAGTTGCCCGAG 500
2083 CAGAAAGTAAAGTTGCCCGAG 2102

RESULT 15
CVU47322
LOCUS          2913 bp      DNA      circular SYN 17-FEB-1996
DEFINITION    Cloning vector DNA, complete sequence.
ACCESSION    U47322
VERSION      U47322.1 GI:1197727
KEYWORDS      unidentified cloning vector
SOURCE        unidentified cloning vector
ORGANISM      other sequences; artificial sequences; vectors.
REFERENCE     1 (bases 1 to 2913)
AUTHORS       Edman,J.C., Clauser,E. and Ellis,L.
TITLE         Direct Submission
JOURNAL       Submitted (26-JAN-1996) J. C. Edman, Hormone Research Institute,
              University of California, San Francisco, Box 0534, San Francisco,
              CA 94143-0534, USA
FEATURES      Location/Qualifiers
source        1. .2913
              /organism="unidentified cloning vector"
              /mol_type="genomic DNA"
              /db_xref="taxon:45196"

ORIGIN
Query Match          92.4%; Score 462; DB 12; Length 2913;
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
1490 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 1549
61 GCGATCTGCTATTCGTTTCATCCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT 120
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|||||
Db 1550 GCCATCTGCTATTTCGTTTCAT-CCATAGTTGCCTG--ACTCCCCGTCGTAGATAACT 1606
QY 121 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTCTGCAATGATACCGCGAAGACCCACG 180
Db 1607 ACCGATACGGAGGGCTTACCATCTGGCCCCAGTGTCTGCAATGATACCGCG-AGACCCACG 1665
QY 181 CTCACGGCTCCAGATTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAG 240
Db 1666 CTCACGGCTCCAGATTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAG 1725
QY 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTGTTGCCGGAAGCTAGAGT 300
Db 1726 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTGTTGCCGGAAGCTAGAGT 1785
QY 301 AAGTAGTTCCGCCAGTTAATAGTTTGGCCAAAGTTGTTGCCATTGCTGCAGGCATCGTGGT 360
Db 1786 AAGTAGTTCCGCCAGTTAATAGTTTGGCCAAAGTTGTTGCCATTGCTGCAGGCATCGTGGT 1845
QY 361 GTCACGCTCGTGTGTTGGTATGGCTTCATTTCAGCTCCGGTCCCAAGCATCAAGGCGAGT 420
Db 1846 GTCACGCTCGTGTGTTGGTATGGCTTCATTTCAGCTCCGGTCCCAAGCATCAAGGCGAGT 1905
QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTAGCTCCTTCGTTCCGATCGTTGT 480
Db 1906 TACATGATCCCCCATGTTGTGCAAAAAGCGGTAGCTCCTTCGTTCCGATCGTTGT 1965
QY 481 CAGAAGTAAGTTGGCGCAG 500
Db 1966 CAGAAGTAAGTTGGCGCAG 1985

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Search completed: April 29, 2005, 04:24:22
Job time : 2579 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 18:49:09 ; Search time 425 Seconds
(without alignments)
6964.402 Million cell updates/sec

Title: US-10-043-160-5_COPY_1_500

Perfect score: 500

Sequence: 1 atatagtgtaaaacttggtc.....cagaagtaagtggcgccgag 500

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	100.0	43226	2	AAX60263 Nucleic a
2	462	92.4	1086	4	AAS41818 DNA seque
3	462	92.4	2022	4	AAS41766 Genomic s
4	462	92.4	2022	4	AAS41810 Genomic s
5	462	92.4	2022	4	AAS41859 Genomic s
6	462	92.4	2022	4	AAS41859 Genomic s
7	462	92.4	2022	4	AAS41859 Genomic s
8	462	92.4	2022	4	AAS41859 Genomic s
9	462	92.4	2022	4	AAS41859 Genomic s
10	462	92.4	2022	4	AAS41859 Genomic s
11	462	92.4	2022	4	AAS41859 Genomic s
12	462	92.4	2022	4	AAS41859 Genomic s
13	462	92.4	2022	4	AAS41859 Genomic s
14	462	92.4	2022	4	AAS41859 Genomic s
15	462	92.4	2022	4	AAS41859 Genomic s
16	462	92.4	2022	4	AAS41859 Genomic s
17	462	92.4	2022	4	AAS41859 Genomic s
18	462	92.4	2022	4	AAS41859 Genomic s
19	462	92.4	2022	4	AAS41859 Genomic s
20	462	92.4	2022	4	AAS41859 Genomic s

C 21	462	92.4	2213	4	AAS41818	Aas41818	Genomic s
C 22	462	92.4	2213	4	AAS41867	Aas41867	Genomic s
C 23	462	92.4	2213	4	AAS41776	Aas41776	Genomic s
C 24	462	92.4	2213	4	AAK85447	Aak85447	Human imm
C 25	462	92.4	2213	4	AAK85447	Aak85447	Human imm
C 26	462	92.4	2213	4	AAK85447	Aak85447	Human imm
C 27	462	92.4	2213	4	AAK85446	Aak85446	Human imm
C 28	462	92.4	2213	4	AAK85496	Aak85496	Human imm
C 29	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 30	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 31	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 32	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 33	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 34	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 35	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 36	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 37	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 38	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 39	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 40	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 41	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 42	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 43	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 44	462	92.4	2213	4	AAK85497	Aak85497	Human imm
C 45	462	92.4	2213	4	AAK85497	Aak85497	Human imm

ALIGNMENTS

RESULT 1

AAX60263

ID AAX60263 standard; DNA; 43226 BP.

XX AAX60263;

AC AAX60263;

XX AAX60263;

DT 12-AUG-1999 (first entry)

XX Nucleic acid sequence from C121 gene of system B of chicken MHC.

DE Resistance: tumour development; Marek disease tumour; chicken; system B;

KW system RFP-Y; poultry major histocompatibility complex; MHC;

KW class II B-L gene; gene 17.5; gene 12.3; gene B-FIV; class I; genotype;

KW selection; breeding; virus-induced tumour; C121 gene; ss.

XX Gallus sp.

OS Gallus sp.

XX FR2771422-A1.

DN FR2771422-A1.

XX 28-MAY-1999.

XX 21-NOV-1997; 97FR-00014669.

XX 21-NOV-1997; 97FR-00014669.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX WPI; 1999-329699/28.

XX Chicken nucleic acid involved in controlling tumor susceptibility.

XX Claim 2; Fig 5; 49pp; French.

XX The specification describes nucleic acid sequences from genes (or related

regions) that encode proteins involved in controlling resistance or

susceptibility to development of tumours (e.g. Marek disease tumours) in

chickens. The nucleic acid sequences include sequences from genes of

systems B or RFP-Y of the poultry major histocompatibility complex (MHC),

other than genes of class II B-L and genes 17.5, 12.3 or B-FIV of class

I. The nucleic acid sequences are used to genotype poultry, particularly

to select (for breeding) birds resistant to virus-induced tumours. The

present sequence represents a nucleic acid sequence from a gene of system

B

XX DE Genomic sequence #82 encoding novel human enzyme polypeptide.
XX
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ds.
XX
XX Homo sapiens.
XX
XX WO200155301-A2.
XX
XX 02-AUG-2001.
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XX 17-JAN-2001; 2001WO-US001239.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
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PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR 25-SEP-2000; 2000US-0234997P.
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PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236368P.
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PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239355P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
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PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
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PR 01-NOV-2000; 2000US-0241826P.
PR 08-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
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PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
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PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
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PR 01-DEC-2000; 2000US-0249300P.
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PR 05-DEC-2000; 2000US-0250391P.
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PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-465566/50.
 XX
 XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,
 PT treating neural, immune system, muscular, reproductive, pulmonary,
 PT cardiovascular, renal, proliferative disorders and cancerous diseases.
 XX
 XX Disclosure; SEQ ID NO 1892; 1180pp; English.
 XX
 XX The present invention relates to the isolation of novel human enzyme
 CC polypeptides (AAU22915-AAU2314), and the cDNA and genomic sequences
 CC encoding them. The enzyme polypeptides of the invention may comprise the
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
 CC isomerases or ligases. The sequences of the invention are useful in the
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of
 CC disorders including hyperproliferative disorders (e.g. cancer),
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
 CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
 CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
 CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
 CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
 CC infectious disorders (e.g. influenza). The polynucleotides of the
 CC invention can also be used in gene therapy. AAS41685-AAS42192 represent
 CC DNA sequences encoding for the novel human enzyme polypeptides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2022 BP; 513 A; 478 C; 512 G; 518 T; 0 U; 1 Other;
 Query Match 92.4%; Score 462; DB 4; Length 2022;
 Best Local Similarity 99.2%; Pred. No. 6.6e-112;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
 1 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTATCAGTGGGACCTATCTCA 60
 1095 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTATCAGTGGGACCTATCTCA 1036
 61 GCGATCTGCTATTTGCTTCACTCCATAGTTGCTGCAACTCCCGTCGTGTAGATAACT 120
 1035 GCGATCTGCTATTTGCTTCACTCCATAGTTGCTGCAACTCCCGTCGTGTAGATAACT 979
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 978 ACGATACGGAGGGCTTACCATCTGGCCCGCCAGTCTGCAATGATACCGGAGCCCAAG 920
 181 CTCACGGCTCCAGATTATCAGCAATAAACACGACGCGGAGGCGGCGGAGGAGGAG 240
 919 CTCACGGCTCCAGATTATCAGCAATAAACACGACGCGGAGGCGGCGGAGGAGGAG 860
 241 TGGTCTGCAACTTTATCCGCTTCACTCCAGTCTTATTAATTTGTCGGGAAAGTAGAGT 300
 859 TGGTCTGCAACTTTATCCGCTTCACTCCAGTCTTATTAATTTGTCGGGAAAGTAGAGT 800
 301 AAGTAGTTGCGCAGTTAATAGTTGCGCAAGGTTGTCGCAATGCTGAGGCGATCGTGGT 360
 799 AAGTAGTTGCGCAGTTAATAGTTGCGCAAGGTTGTCGCAATGCTGAGGCGATCGTGGT 740
 361 GTCAGCTCGTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 420
 739 GTCAGCTCGTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 680

QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCTTTCGGTCTCCGATCGTTGT 480
 DB 679 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCTTTCGGTCTCCGATCGTTGT 620
 QY 481 CAGAAGTAAGTTGGCCGCGAG 500
 DB 619 CAGAAGTAAGTTGGCCGCGAG 600
 RESULT 4
 AAS41810/c
 ID AAS41810 standard; DNA; 2022 BP.
 XX
 AC AAS41810;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Genomic sequence #126 encoding novel human enzyme polypeptide.
 XX
 KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
 KW ligase; hyperproliferative disorder; immunodeficiency disorder;
 KW autoimmune disorder; neurological disorder; metabolic disorder;
 KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
 KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
 KW anti arthritic; nephrotropic; anticoagulant; ds.
 XX
 OS Homo sapiens.
 XX
 FN WO200155301-A2.
 XX
 PD 02-AUG-2001.
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 XX 17-JAN-2001; 2001WO-US001239.
 PR 31-JAN-2000; 2000US-0179065P.
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PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
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PR 29-SEP-2000; 2000US-0236327P.
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PR 02-OCT-2000; 2000US-0236802P.
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PR 13-OCT-2000; 2000US-0239335P.
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PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
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PR 20-OCT-2000; 2000US-0241787P.
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PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 01-NOV-2000; 2000US-0244617P.
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PR 08-NOV-2000; 2000US-0246477P.
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PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
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PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.
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PR 17-NOV-2000; 2000US-0249277P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
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PR 08-DEC-2000; 2000US-0251868P.
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PR 08-DEC-2000; 2000US-0251989P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 03-JAN-2001; 2001US-0259678P.

XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX
XX WPI; 2001-465566/50.
DR
XX
XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Disclosure; SEQ ID NO 1936; 1180pp; English.

XX
XX The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC infectious disorders (e.g. Influenza). The polynucleotides of the
CC invention can also be used in gene therapy. AAS41685-AAS42192 represent
CC DNA sequences encoding for the novel human enzyme polypeptides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2022 BP; 513 A; 478 C; 512 G; 518 T; 0 U; 1 Other;

Query Match 92.4%; Score 462; DB 4; Length 2022;
Best Local Similarity 99.2%; Pred. NO. 6.6e-112;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTCAGGACCATCTCTCA 60
|||||
Db 1095 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTCAGGACCATCTCTCA 1036
|||||

QY 61 GCGATCTGCTATTTCGTTTCATCCCATAGTTCCTCCAACTCCCGTCGTAGATAAAT 120
|||||
Db 1035 GCGATCTGCTATTTCGTTTCAT-CCATAGTTCCTG-ACCTCCCGTCGTAGATAAAT 979
|||||

QY 121 ACATACGGAGGGCTTACCATCTGCCCCAGTCGTGCAATGATACCGGAGACCCACG 180
|||||

978	Qy	ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTCTGCAATGATACGGG-AGACCCACG	920
181	Qy	CTCACGGCTCCAGATTTATCAGCAATAAACACGACCGGAGCGGAGCGCAGAG	240
919	Db	CTCACGGCTCCAGATTTATCAGCAATAAACACGACCGGAGCGGAGCGCAGAG	860
241	Qy	TGCTCTCGCAACTTTTATCGGCTCCATCCAGTCTATTAAATTGTGCGGGAAGCTAGGT	300
859	Db	TGGTCTCTGCAACTTTTATCGGCTCCATCCAGTCTATTAAATTGTGCGGGAAGCTAGGT	800
301	Qy	AAGTAGTTCCGCGAGTTAATAGTTTTCGCGCAAGTTGTTGCCATTGCTCTCAGGCATCTCGGT	360
799	Db	AAGTAGTTCCGCGAGTTAATAGTTTTCGCGCAAGTTGTTGCCATTGCTCTCAGGCATCTCGGT	740
361	Qy	GTACAGCTCGTGTGTTGGTATGGCTTCATTACAGTCCGGTTCCCAAGCATCAAGGCGAGT	420
739	Db	GTACAGCTCGTGTGTTGGTATGGCTTCATTACAGTCCGGTTCCCAAGCATCAAGGCGAGT	680
421	Qy	TACATGATCCCCCATGTTGTGCAAAAAAGCGTTAGCTCCTTCGGTCTCCCGATCGTTGT	480
679	Db	TACATGATCCCCCATGTTGTGCAAAAAAGCGTTAGCTCCTTCGGTCTCCCGATCGTTGT	620
481	Qy	CAGAAGTAAGTTGGCCGAC	500
619	Db	CAGAAGTAAGTTGGCCGAC	600

RESULT 5	
AAS41859/c	
ID AAS41859	standard; DNA; 2022 BP.
XX	
XX AC	AAS41859;
XX	
XX DT	17-DEC-2001 (first entry)
XX	
DE	Genomic sequence #175 encoding novel human enzyme polypeptide.
XX	
XX KW	Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
XX KW	ligase; hyperproliferative disorder; immunodeficiency disorder;
XX KW	autoimmune disorder; neurological disorder; metabolic disorder;
XX KW	inflammatory disorder; cardiovascular disorder; reproductive disorder;
XX KW	blood-related disorder; infectious disorder; gene therapy; cytostatic;
XX KW	anti arthritic; nephrotropic; anticoagulant; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200155301-A2.
XX	
PD	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US001239.
XX	
PR	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214886P.
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PR	07-JUL-2000; 2000US-0216647P.
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PR 08-NOV-2000; 2000US-0246524P.
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 PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Baraash SC, Ruben SM;

XX WPI; 2001-465566/50.

XX Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

XX Disclosure; SEQ ID NO 1985; 1180pp; English.

XX The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. AA541685-AA542192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 2022 BP; 513 A; 478 C; 512 G; 518 T; 0 U; 1 Other;
 Query Match 92.4%; Score 462; DB 4; Length 2022;
 Best Local Similarity 99.2%; Pred. No. 6.6e-112;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
 QY 1 ATATATGAGTAAACTTTGGTCTGACAGTTACCAATGCTTAATCATGAGTGAGGACCTATCTCA 60
 DB 1095 ATATATGAGTAAACTTTGGTCTGACAGTTACCAATGCTTAATCATGAGTGAGGACCTATCTCA 1036
 QY 61 GCGATCTGTCTATTTTCGTTTCATCCCATAGTTCGCTGCACTCCCTCCGTTGAGTAACT 120
 DB 1035 GCGATCTGTCTATTTTCGTTTCATCCCATAGTTCGCTGCACTCCCTCCGTTGAGTAACT 979
 QY 121 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTCTGCAATGATACCGCGAAGACCCACG 180
 DB 978 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTCTGCAATGATACCGCG-AGACCCACG 920
 QY 181 CTCACCGGCTCCAGATTTTATCAGCAATAAACCCAGCCGCGGAGGCGGCGCAGAGAAG 240
 DB 919 CTCACCGGCTCCAGATTTTATCAGCAATAAACCCAGCCGCGGAGGCGGCGCAGAGAAG 860
 QY 241 TGGTCTCTGCAACTTTTATCCGCTCCATCCAGTCTATTAATTGTTGCGGGAAGCTAGAGT 300
 DB 859 TGGTCTCTGCAACTTTTATCCGCTCCATCCAGTCTATTAATTGTTGCGGGAAGCTAGAGT 800
 QY 301 AAGTAGTTCCGCAAGTTAATAGTTTGGCAACGTTGTTGCCATTGCTGCAGGCATCGTGT 360
 DB 799 AAGTAGTTCCGCAAGTTAATAGTTTGGCAACGTTGTTGCCATTGCTGCAGGCATCGTGT 740
 QY 361 GTCACGCTCGTCTGTTGGTATGCGCTTCATTTCAGCTCCGGTTCCTCCAAACGATCAAGGCGAGT 420
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 QY 421 TACATGATCCCCCATGTTGTGCAAAAAAGGGTTAGCTCTCTCGGTCCTCCGATCGTGT 480
 DB 679 TACATGATCCCCCATGTTGTGCAAAAAAGGGTTAGCTCTCTCGGTCCTCCGATCGTGT 620
 QY 481 CAGAAGTAAAGTTGGCGGCAG 500
 DB 619 CAGAAGTAAAGTTGGCGGCAG 600
 RESULT 6
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 ID AAK69615 standard; DNA; 2022 BP.
 XX AC AAK69615;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24427.
 XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX OS Homo sapiens.
 XX XX WO200157182-A2.
 XX PD 09-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US001354.
 XX PR 31-JAN-2000; 2000US-0179065P.
 XX PR 04-FEB-2000; 2000US-0180628P.
 XX PR 24-FEB-2000; 2000US-0184664P.
 XX PR 02-MAR-2000; 2000US-0186350P.
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 XX PR 17-MAR-2000; 2000US-0190076P.
 XX PR 18-APR-2000; 2000US-0198123P.
 XX PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-02559678P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-483426/52.
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and metastasis.
Disclosure; SEQ ID NO 24427; 3071pp + Sequence Listing; English.
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased

CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 XX Sequence: 2022 BP; 513 A; 478 C; 512 G; 518 T; 0 U; 1 Other;

Query Match 92.4%; Score 462; DB 4; Length 2022;
 Best Local Similarity 99.2%; Pred. No. 6.6e-112;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
 QY 1 ATATATCAGTAACCTTGGTCTGACAGTTACCAATGCTTAATCAGTAGGACCTATCTCA 60
 DB 1095 ATATATCAGTAACCTTGGTCTGACAGTTACCAATGCTTAATCAGTAGGACCTATCTCA 1036
 QY 61 GCGATCTGTCTATTTCGTTTCATCCATAGTTGCTGCAACTCCCGTCGTTAGATAACT 120
 DB 1035 GCGATCTGTCTATTTCGTTTCAT-CCATAGTTGCTG--ACTCCCGTCGTTAGATAACT 979
 QY 121 ACGATACGGGAGGGCTTACCATCTGCGCCCGAGTGTCAATGATACCGGAAGACCCACG 180
 DB 978 ACGATACGGGAGGGCTTACCATCTGCGCCCGAGTGTCAATGATACCGG-AGACCCACG 920
 QY 181 CTCACGGCTCCAGATTATCAGCAATAAACAGCCAGCGGGAAGGCCGAGCGAGAAG 240
 DB 919 CTCACGGCTCCAGATTATCAGCAATAAACAGCCAGCGGGAAGGCCGAGCGAGAAG 860
 QY 241 TGTCTCTGCACTTATCCGCTCCATCCAGTCTTAATTAATTTGTCGGGAAGCTAGAGT 300
 DB 859 TGTCTCTGCACTTATCCGCTCCATCCAGTCTTAATTAATTTGTCGGGAAGCTAGAGT 800
 QY 301 AAGTAGTTCGCCAGTTAATAGTTTGCACACAGTTGTCGATGCTGCGGCAATCGTGGT 360
 DB 799 AAGTAGTTCGCCAGTTAATAGTTTGCACACAGTTGTCGATGCTGCGGCAATCGTGGT 740
 QY 361 GTCACGCTCGTCTGTTGGTATGGCTTCATTCAGTCCGTTCCCAACGATCAAGGGGAGT 420
 DB 739 GTCACGCTCGTCTGTTGGTATGGCTTCATTCAGTCCGTTCCCAACGATCAAGGGGAGT 680
 QY 421 TACATGATCCCATGTTGTCAAAAGCGTTAGCTCTCTCGTCTCCGATCGTTGT 480
 DB 679 TACATGATCCCATGTTGTCAAAAGCGTTAGCTCTCTCGTCTCCGATCGTTGT 620
 QY 481 CAGAAGTAAGTTGGCCGCGAG 500
 DB 619 CAGAAGTAAGTTGGCCGCGAG 600

RESULT 7
 ID AAK85438 standard; DNA; 2022 BP.
 XX AAK85438;
 AC AAK85438;
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 XX 07-NOV-2001 (first entry)
 DT
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40250.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX
 QS Homo sapiens.
 XX
 PN W0200157182-A2.
 XX
 PD 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US0001354.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
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 PR 02-MAR-2000; 2000US-0186350P.
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 PR 07-JUN-2000; 2000US-0209467P.
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 PR 08-SEP-2000; 2000US-0231242P.
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 PR 29-SEP-2000; 2000US-0236327P.
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XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40300.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
KW Homo sapiens.
XX W0200157182-A2.
PN 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US001354.
PF 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
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PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
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PR 25-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
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PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
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PR 20-OCT-2000; 2000US-0241809P.
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PR 01-NOV-2000; 2000US-024617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
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PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
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PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249211P.
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PR 17-NOV-2000; 2000US-0249213P.
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PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
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PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.

08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Disclosure; SEQ ID NO 40300; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX SQ Sequence 2022 BP; 513 A; 478 C; 512 G; 518 T; 0 U; 1 Other;
Query Match 92.4%; Score 462; DB 4; Length 2022;
Best Local Similarity 99.2%; Pred. No. 6.6e-112;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCATGTGAGGACCTTCTCA 60
DB 1095 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCATGTGAGGACCTTCTCA 1036
QY 61 GCGATCTGCTTATTTGCTTATCCATCTGCTGCAACTCCCGCTGCTGAGTAACCT 120
DB 1035 GCGATCTGCTTATTTGCTTATCCATCTGCTGCAACTCCCGCTGCTGAGTAACCT 979
QY 121 ACGATACGGAGGGCTTACCATCTGCGCCCGCAGTGTCTGCAATGATACCGGAAGCCACG 180
DB 978 ACGATACGGAGGGCTTACCATCTGCGCCCGCAGTGTCTGCAATGATACCGCG-AGACCCACG 920
QY 181 CTCACCGGCTCCAGTATTTACGCAATTAACACGACGCGGAGGCGCCGAGCAGAG 240
DB 919 CTCACCGGCTCCAGTATTTACGCAATTAACACGACGCGGAGGCGCCGAGCAGAG 860
QY 241 TGGTCTGCACTTTATCCGCTCCATCTGCTTATTAATTTGTCGCGGAAGCTAGAGT 300
DB 859 TGGTCTGCACTTTATCCGCTCCATCTGCTTATTAATTTGTCGCGGAAGCTAGAGT 800
QY 301 AAGTAGTTGCGCAGTAAATAGTTTGGCGCAACGTTTGGTGGCCATGCTGAGGCAATCGTGT 360
DB 799 AAGTAGTTGCGCAGTAAATAGTTTGGCGCAACGTTTGGTGGCCATGCTGAGGCAATCGTGT 740
QY 361 GTCAGCTGCTGCTTGTGATGCTTCAATTCAGCTCGGTTCCCAACGATCAAGGCGAGT 420
DB 739 GTCAGCTGCTGCTTGTGATGCTTCAATTCAGCTCGGTTTCCCAACGATCAAGGCGAGT 680
QY 421 TACATGATCCCGCAGTAAATAGTTTGGCGCAACGTTTGGTGGCCATGCTGAGGCAATCGTGT 480
DB 679 TACATGATCCCGCAGTAAATAGTTTGGCGCAACGTTTGGTGGCCATGCTGAGGCAATCGTGT 620
QY 481 CAGAAAGTAAGTTGGCCGAG 500

DB 619 CAGAAGTAAGTTGGCCGAG 600
RESULT 9
AAAN91727/c
ID AAAN91727 standard; DNA; 2039 BP.
XX AAAN91727;
XX 25-MAR-2003 (revised)
DT 13-APR-1990 (first entry)
XX as Coding strand of a portion of a 7.3 kb Neisseria gonorrhoeae plasmid
DE carrying the beta-lactamase TEM-1 gene.
XX Neisseria gonorrhoeae plasmid; beta-lactamase TEM-1 gene; capture probe;
KW label probe.
XX Neisseria gonorrhoeae.
XX Key Location/Qualifiers
CDS 1..861
/*tag= a
PN WO8903891-A.
XX 05-MAY-1989.
XX 14-OCT-1988; 88WO-US0003644.
XX 15-OCT-1987; 87US-00109282.
PR 22-APR-1988; 88US-00185201.
PR 30-SEP-1988; 88US-00252638.
XX (CHIR) CHIRON CORP.
XX Urdea MS, Warner B, Running JA, Kolberg JA, Clyne JM;
PI Sanchezpaz R, Horn T;
XX WPI; 1989-150787/20.
XX Nucleic acid multimer for hybridisation assays - having single-stranded
PT oligo-nucleotide units capable of binding specifically to sequences of
PT interest.
XX Fig 9; Page ?; 112pp; English.
XX Sandwich hybridisation assays use label probes which are complementary to
CC portions of the CDS (tag a) and capture probes which are complementary to
CC portions which are downstream of the CDS. (Updated on 25-MAR-2003 to
CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
CC on 25-MAR-2003 to correct PI field.)
XX Sequence 2039 BP; 560 A; 437 C; 396 G; 646 T; 0 U; 0 Other;
SQ Query Match 92.4%; Score 462; DB 1; Length 2039;
Best Local Similarity 99.2%; Pred. No. 6.6e-112;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCATGTGAGGACCTTCTCA 60
DB 887 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCATGTGAGGACCTTCTCA 828
QY 61 GCGATCTGCTTATTTGCTTATCCATCTGCTGCAACTCCCGCTGCTGAGTAACCT 120
DB 827 GCGATCTGCTTATTTGCTTATCCATCTGCTGCAACTCCCGCTGCTGAGTAACCT 771
QY 121 ACGATACGGAGGGCTTACCATCTGCGCCCGCAGTGTCTGCAATGATACCGGAAGCCACG 180
DB 770 ACGATACGGAGGGCTTACCATCTGCGCCCGCAGTGTCTGCAATGATACCGCG-AGACCCACG 712
QY 181 CTCACCGGCTCCAGTATTTATCAGCAATAAACACGACGCGGAGGCGCCGAGCAGAG 240

Db 711 CTACCGGCTCCAGATTATCAGCAATAAACCCAGCCAGCGGAGGCGCGAGAG 652
 Qy 241 TGGTCTGCAACTTATCCGCTCCATCCAGTCTATTATTTGTCGGGGAAGCTAGAGT 300
 Db 651 TGGTCTGCAACTTATCCGCTCCATCCAGTCTATTATTTGTCGGGGAAGCTAGAGT 592
 Qy 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACAGTTGTTGCCATTGCTGCAGGCATCGTGGT 360
 Db 591 AAGTAGTTCGCCAGTTAATAGTTTGGCAACAGTTGTTGCCATTGCTGCAGGCATCGTGGT 532
 Qy 361 GTACGCTCGTGGTGGTATGCTTCAATTCAGTCCGGTTCCTCAACGATCAAGGCGAGT 420
 Db 531 GTACGCTCGTGGTGGTATGCTTCAATTCAGTCCGGTTCCTCAACGATCAAGGCGAGT 472
 Qy 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTTGT 480
 Db 471 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTTGT 412
 Qy 481 CAGAAGTAAAGTTGGCCGCGAG 500
 Db 411 CAGAAGTAAAGTTGGCCGCGAG 392

RESULT 10
 AAA14722/c
 ID AAA14722 standard; DNA; 2187 BP.
 XX
 AC AAA14722;
 XX
 DT 06-AUG-2003 (revised)
 DT 08-AUG-2000 (first entry)
 XX
 DE Nucleotide sequence of region A of vector Ad5RSVbeta-lactamase.
 XX
 KW Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;
 KW replication-deficient adenovirus type 5; suicide gene therapy;
 KW cancer cell; chemotherapy; beta-lactamase produg enzyme; produg TCM;
 KW anticancer; tumor; leukemia; breast cancer; Wilm's tumor;
 KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;
 KW papillary adenocarcinoma; ss.
 XX
 OS Synthetic.
 OS Rous sarcoma virus.
 OS Mastadenovirus.
 XX
 PN WO200020608-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 01-OCT-1999; 99WO-US020908.
 XX
 PR 02-OCT-1998; 98US-00165321.
 XX
 PA (GENO-) GENOTHERAPEUTICS INC.
 XX
 PI Steiner MS;
 XX
 DR WPI; 2000-303788/26.
 XX
 PT Treating cancer using viral vectors which encode enzymes that convert
 PT inactive drugs to active cytotoxic agents, expression of the enzyme is
 PT tissue specific therefore targeting the effects of the drug to tumor
 PT cells.
 XX
 PS Disclosure; Fig 10; 130pp; English.
 XX
 CC The specification describes a method for inducing cellular cytotoxicity
 CC in tumor cells using replication-deficient adenovirus type 5 expression
 CC vectors. The vectors comprise a sequence encoding a beta-lactamase under
 CC the control of a Rous Sarcoma virus in combination with a produg
 CC conjugated to a toxic agent. Tissue specific expression of the enzyme
 CC converts the inactive drugs into active cancer killing agents. The

adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-lactamase sequence is inserted within this region. The vectors are used for suicide gene therapy. This involves introducing genes into cancer cells that encode enzymes capable of converting inactive drugs into active cancer killing agents. If tissue specific promoters are coupled to the produg enzymes, then production of the produg will be tissue specific and targeted to the tumor. Therefore the cancer cells act as their own factories to activate chemotherapy agents and commit suicide. Beta-lactamase produg enzymes convert produg TCM into an active anticancer agent which is cytotoxic to cancer cells PPC-1. The method is used to treat patients with cancers of the brain, bladder or prostate. It may also be used to treat a range of other tumors such as leukemia, breast cancer, Wilm's tumor, small cell lung carcinoma, Ewing's sarcoma, colon carcinoma and papillary adenocarcinomas. The present sequence represents region A of vector Ad5RSVbeta-lactamase, a vector of the CC invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 2187 BP; 562 A; 477 C; 592 G; 556 T; 0 U; 0 Other;

Query Match 92.4%; Score 462; DB 3; Length 2187;
 Best Local Similarity 99.2%; Pred. No. 6.6e-112;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
 Qy 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCA 60
 Db 1993 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCA 1934
 Qy 61 GCATCTGCTATTTCGTTTCATCCCATAGTTGCTGCAATCCCGCTCGTGTAGATAACT 120
 Db 1933 GCATCTGCTATTTCGTTTCAT-CCATAGTTGCTG--ACTCCCGCTCGTGTAGATAACT 1877
 Qy 121 ACGATACGGAGGGCTTACCATCTGCCCCAGTGTGCAATGATACCGCAAGACCCACG 180
 Db 1876 ACGATACGGAGGGCTTACCATCTGCCCCAGTGTGCAATGATACCGCG-AGACCCACG 1818
 Qy 181 CTCACGGCTCCAGATTATCAGCAATNACCCAGCCGAGGCGGAGCGCAGAG 240
 Db 1817 CTCACGGCTCCAGATTATCAGCAATNACCCAGCCGAGGCGGAGCGCAGAG 1758
 Qy 241 TGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 300
 Db 1757 TGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 1698
 Qy 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACAGTTGTTGCCATTGCTGCAGGCATCGTGGT 360
 Db 1697 AAGTAGTTCGCCAGTTAATAGTTTGGCAACAGTTGTTGCCATTGCTGCAGGCATCGTGGT 1638
 Qy 361 GTACGCTCGTGGTGGTATGCTTCAATTCAGTCCGGTTCCTCCCAACGATCAAGGCGAGT 420
 Db 1637 GTACGCTCGTGGTGGTATGCTTCAATTCAGTCCGGTTCCTCCCAACGATCAAGGCGAGT 1578
 Qy 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTTGT 480
 Db 1577 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTTGT 1518
 Qy 481 CAGAAGTAAAGTTGGCCGCGAG 500
 Db 1517 CAGAAGTAAAGTTGGCCGCGAG 1498

RESULT 11
 AAS41826/c
 ID AAS41826 standard; DNA; 2212 BP.
 XX
 AC AAS41826;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Genomic sequence #142 encoding novel human enzyme polypeptide.
 XX
 KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
 KW ligase; hyperproliferative disorder; immunodeficiency disorder;
 KW autoimmune disorder; neurological disorder; metabolic disorder;

* inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ds.

XX Homo sapiens.

PN WO200155301-A2.

XX 02-AUG-2001.

PD 17-JAN-2001; 2001WO-US001239.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220363P.

PR 26-JUL-2000; 2000US-0220364P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226686P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 05-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232337P.

PR 14-SEP-2000; 2000US-0232338P.

PR 14-SEP-2000; 2000US-0232339P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0232406P.

PR 14-SEP-2000; 2000US-0233064P.

PR 21-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246533P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249210P.

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PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.

PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.

PR 17-NOV-2000; 2000US-0249218P.

PR 17-NOV-2000; 2000US-0249244P.

PR 17-NOV-2000; 2000US-0249245P.

PR 17-NOV-2000; 2000US-0249246P.

PR 17-NOV-2000; 2000US-0249265P.

PR 17-NOV-2000; 2000US-0249266P.

PR 17-NOV-2000; 2000US-0249297P.

PR 17-NOV-2000; 2000US-0249299P.

PR 01-DEC-2000; 2000US-0250160P.

PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.

PR 05-DEC-2000; 2000US-0251988P.

PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251869P.

PR 08-DEC-2000; 2000US-0251989P.

PR 08-DEC-2000; 2000US-0251990P.

PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-465566/50.
 XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,
 PT treating neural, immune system, muscular, reproductive, pulmonary,
 PT cardiovascular, renal, proliferative disorders and cancerous diseases.
 XX Disclosure; SEQ ID NO 1952; 1180pp; English.
 XX The present invention relates to the isolation of novel human enzyme
 CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
 CC encoding them. The enzyme polypeptides of the invention may comprise the
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
 CC isomerases or ligases. The sequences of the invention are useful in the
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of
 CC disorders including hyperproliferative disorders (e.g. cancer),
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
 CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
 CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
 CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
 CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
 CC infectious disorders (e.g. influenza). The polynucleotides of the
 CC invention can also be used in gene therapy. AAS41685-AAS42192 represent
 CC DNA sequences encoding for the novel human enzyme polypeptides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 2212 BP; 558 A; 537 C; 557 G; 560 T; 0 U; 0 Other;
 SQ

Query Match 92.4%; Score 462; DB 4; Length 2212;
 Best Local Similarity 99.2%; Pred. No. 6.6e-112;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

QY 1 ATATATGAGTAACTTGGTCTGACAGTACCAATGCTTAATCAGTGGGACCTTCTCA 60
 DB 1098 ATATATGAGTAACTTGGTCTGACAGTACCAATGCTTAATCAGTGGGACCTTCTCA 1039
 QY 61 GCATCTGCTCTATTTCGTTCCATCCCATAGTTCCTGCACTCCCGTCTGTAGATAACT 120
 DB 1038 GCATCTGCTCTATTTCGTTCCATCCCATAGTTCCTGCACTCCCGTCTGTAGATAACT 982
 QY 121 ACATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAAGACCCACG 180
 DB 981 ACATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGG-AGACCCACG 923
 QY 181 CTCACGGCTCCAGATTATCAGCAATAAACACGACCGCGGAGGCGGCGGCGGAGG 240
 DB 922 CTCACGGCTCCAGATTATCAGCAATAAACACGACCGCGGAGGCGGCGGCGGAGG 863
 QY 241 TGTCTCTGCAACTTTATCCGCTCCATCCAGTCTTATTAATTTGTCGGGAAGCTAGAGT 300
 DB 862 TGTCTCTGCAACTTTATCCGCTCCATCCAGTCTTATTAATTTGTCGGGAAGCTAGAGT 803
 QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT 360
 DB 802 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT 743
 QY 361 GTCACGCTCGTGGTGGTAGGTTCAATTCAGTTCGGTTCCCAAGATCAAGGCGAGT 420
 DB 742 GTCACGCTCGTGGTGGTAGGTTCAATTCAGTTCGGTTCCCAAGATCAAGGCGAGT 683
 QY 421 TACATGATCCCATGTTGTCGCAAAAGCGGTTAGCTCTCGTCTCGGATCGTTGT 480
 DB 682 TACATGATCCCATGTTGTCGCAAAAGCGGTTAGCTCTCGTCTCGGATCGTTGT 623
 QY 481 CAGAAGTAGTTCGCCGCGAG 500

Db 622 CAGAGTAAGTTGGCGCAG 603
 RESULT 12
 AAS41782/c
 ID AAS41782 standard; DNA; 2212 BP.
 XX AC AAS41782;
 XX DT 17-DEC-2001 (first entry)
 XX DE Genomic sequence #98 encoding novel human enzyme polypeptide.
 XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
 KW ligase; hyperproliferative disorder; immunodeficiency disorder;
 KW autoimmune disorder; neurological disorder; metabolic disorder;
 KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
 KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
 KW anti arthritic; nephrotropic; anticoagulant; ds.
 XX Homo sapiens.
 OS
 XX WO200153301-A2.
 XX 02-AUG-2001.
 XX 17-JAN-2001; 2001WO-US001239.
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225477P.
 PR 14-AUG-2000; 2000US-0225757P.
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 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
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 PR 23-AUG-2000; 2000US-0227009P.
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 PR 01-SEP-2000; 2000US-0229343P.
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 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.

AA	17-JAN-2001;	2001WO-US0001239.
PF		
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PR	31-JAN-2000;	2000US-0179065P.
PR	04-FEB-2000;	2000US-0180628P.
PR	24-FEB-2000;	2000US-0184664P.
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PR	16-MAR-2000;	2000US-0198874P.
PR	17-MAR-2000;	2000US-0190076P.
PR	18-APR-2000;	2000US-0198123P.
PR	19-MAY-2000;	2000US-0205515P.
PR	07-JUN-2000;	2000US-0209467P.
PR	28-JUN-2000;	2000US-0214886P.
PR	30-JUN-2000;	2000US-0215135P.
PR	07-JUL-2000;	2000US-0216647P.
PR	17-JUL-2000;	2000US-0216980P.
PR	11-JUL-2000;	2000US-0217487P.
PR	11-JUL-2000;	2000US-0217496P.
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PR	14-AUG-2000;	2000US-0224518P.
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PR	14-AUG-2000;	2000US-0225214P.
PR	14-AUG-2000;	2000US-0225266P.
PR	14-AUG-2000;	2000US-0225267P.
PR	14-AUG-2000;	2000US-0225268P.
PR	14-AUG-2000;	2000US-0225270P.
PR	14-AUG-2000;	2000US-0225447P.

PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-465566/50.
 XX
 PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,
 PT treating neural, immune system, muscular, reproductive, pulmonary,
 PT cardiovascular, renal, proliferative disorders and cancerous diseases.
 XX
 XX Disclosure; SEQ ID NO 2001; 1180pp; English.
 XX
 CC The present invention relates to the isolation of novel human enzyme
 CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
 CC encoding them. The enzyme polypeptides of the invention may comprise the
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
 CC isomerases or ligases. The sequences of the invention are useful in the
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of
 CC disorders including hyperproliferative disorders (e.g. cancer),
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
 CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
 CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
 CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
 CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
 CC infectious disorders (e.g. influenza). The polynucleotides of the
 CC invention can also be used in gene therapy. AAS41685-AAS42192 represent
 CC DNA sequences encoding for the novel human enzyme polypeptides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2212 BP; 558 A; 537 C; 557 G; 560 T; 0 U; 0 Other;
 Query Match 92.4%; Score 462; DB 4; Length 2212;
 Best Local Similarity 99.2%; Pred. No. 6.6e-112;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

QY	1	ATATATGAGTAACCTTGGTCTGACAGTTACCAATGCTTAATCAGTCAGGACCACTATCTCA	60
DB	1098	ATATATGAGTAACCTTGGTCTGACAGTTACCAATGCTTAATCAGTCAGGACCACTATCTCA	1039
QY	61	GGGATCTGTCTATTTTCGTTTCATCCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT	120
DB	1038	GGGATCTGTCTATTTTCGTTTCATCCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT	982
QY	121	ACGATACGGGAGGGCTTACCATCTGCGCCCAAGTGTGCAATGATACCGGAGACCCACG	180
DB	981	ACGATACGGGAGGGCTTACCATCTGCGCCCAAGTGTGCAATGATACCGGAGACCCACG	923
QY	181	CTCACCGGCTCCAGATTTTATCAGCAATAAACCCAGCCGGAAGGCGGAGCGCAGAG	240
DB	922	CTCACCGGCTCCAGATTTTATCAGCAATAAACCCAGCCGGAAGGCGGAGCGCAGAG	863
QY	241	TGGTCTCTGCAACTTTTATCCGCTCCATCCAGTCTTATTAATTGTTGCCGGAAGCTAGAGT	300
DB	862	TGGTCTCTGCAACTTTTATCCGCTCCATCCAGTCTTATTAATTGTTGCCGGAAGCTAGAGT	803
QY	301	AAGTAGTTCCGAGTTAATAGTTTGGCGAAAGTGTGCAATGCTGCAAGGCATCTGTT	360
DB	802	AAGTAGTTCCGAGTTAATAGTTTGGCGAAAGTGTGCAATGCTGCAAGGCATCTGTT	743
QY	361	GTCACGCTCGTGTGGTATGCTTTCATTTCAGCTCCGCTTCCCAACGATCAAGGCGAGT	420
DB	742	GTCACGCTCGTGTGGTATGCTTTCATTTCAGCTCCGCTTCCCAACGATCAAGGCGAGT	683
QY	421	TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTTCGGTCTCCGATCGTTGT	480
DB	682	TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTTCGGTCTCCGATCGTTGT	623
QY	481	CAGAAGTAAGTTGGCGGCGAG	500
DB	622	CAGAAGTAAGTTGGCGGCGAG	603
RESULT 14			
AAK85505/c			
ID	AAK85505 standard; DNA; 2212 BP.		
AC	AAK85505;		
XX			
DT	07-NOV-2001 (first entry)		
XX			
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40317.		
XX			
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cytostatic; gene therapy; vaccine; metastasis; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200157182-A2.		
XX			
PD	09-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US001354.		
XX			
PR	31-JAN-2000; 2000US-0179065P.		
PR	04-FEB-2000; 2000US-0180628P.		
PR	24-FEB-2000; 2000US-0184664P.		
PR	02-MAR-2000; 2000US-0186350P.		
PR	16-MAR-2000; 2000US-0189874P.		
PR	17-MAR-2000; 2000US-0190076P.		
PR	18-APR-2000; 2000US-0198123P.		
PR	19-MAY-2000; 2000US-0205515P.		
PR	07-JUN-2000; 2000US-0209467P.		
PR	28-JUN-2000; 2000US-0214886P.		
PR	30-JUN-2000; 2000US-0215135P.		
PR	07-JUL-2000; 2000US-0216647P.		
PR	07-JUL-2000; 2000US-0216880P.		
PR	11-JUL-2000; 2000US-0217487P.		

PR	01-NOV-2000;	2000US-0244617P.
PR	08-NOV-2000;	2000US-0246474P.
PR	08-NOV-2000;	2000US-0246475P.
PR	08-NOV-2000;	2000US-0246476P.
PR	08-NOV-2000;	2000US-0246477P.
PR	08-NOV-2000;	2000US-0246478P.
PR	08-NOV-2000;	2000US-0248523P.
PR	08-NOV-2000;	2000US-0248524P.
PR	08-NOV-2000;	2000US-0248525P.
PR	08-NOV-2000;	2000US-0248526P.
PR	08-NOV-2000;	2000US-0248527P.
PR	08-NOV-2000;	2000US-0248528P.
PR	08-NOV-2000;	2000US-0248532P.
PR	08-NOV-2000;	2000US-0248609P.
PR	08-NOV-2000;	2000US-0248610P.
PR	08-NOV-2000;	2000US-0248611P.
PR	08-NOV-2000;	2000US-0248613P.
PR	17-NOV-2000;	2000US-0249207P.
PR	17-NOV-2000;	2000US-0249208P.
PR	17-NOV-2000;	2000US-0249209P.
PR	17-NOV-2000;	2000US-0249210P.
PR	17-NOV-2000;	2000US-0249211P.
PR	17-NOV-2000;	2000US-0249212P.
PR	17-NOV-2000;	2000US-0249213P.
PR	17-NOV-2000;	2000US-0249214P.
PR	17-NOV-2000;	2000US-0249215P.
PR	17-NOV-2000;	2000US-0249216P.
PR	17-NOV-2000;	2000US-0249217P.
PR	17-NOV-2000;	2000US-0249218P.
PR	17-NOV-2000;	2000US-0249244P.
PR	17-NOV-2000;	2000US-0249245P.
PR	17-NOV-2000;	2000US-0249264P.
PR	17-NOV-2000;	2000US-0249265P.
PR	17-NOV-2000;	2000US-0249297P.
PR	17-NOV-2000;	2000US-0249299P.
PR	17-NOV-2000;	2000US-0249300P.
PR	01-DEC-2000;	2000US-0250160P.
PR	01-DEC-2000;	2000US-0250391P.
PR	05-DEC-2000;	2000US-0251030P.
PR	05-DEC-2000;	2000US-0251988P.
PR	05-DEC-2000;	2000US-0256719P.
PR	06-DEC-2000;	2000US-0251479P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	08-DEC-2000;	2000US-0251990P.
PR	11-DEC-2000;	2000US-0254097P.
PR	05-JAN-2001;	2001US-0259678P.
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX		
XX	Rosen CA, Barash SC, Ruben SM;	
PI		
PI		
XX		
XX	WPI; 2001-483426/52.	
DR		
XX		
XX	Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.	
PT		
PT		
XX		
XX	Disclosure; SEQ ID NO 40317; 307lpp + Sequence Listing; English.	
XX		
XX		
CC	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM92170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins, and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. (I) expression, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent,	

CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK67694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 2212 BP; 558 A; 537 C; 557 G; 560 T; 0 U; 0 Other;

Query Match 92.4%; Score 462; DB 4; Length 2212;
 Best Local Similarity 99.2%; Pred. No. 6.6e-112;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
 Qy 1 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGGACCTATCTCA 60
 Db 1098 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGGACCTATCTCA 1039
 Qy 61 GCGATCTGTCTATTTGTTTCCATCCATGCTGCAACTCCCGTGGTAGATAACT 120
 Db 1038 GCGATCTGTCTATTTGTTTCCATCCATGCTGCAACTCCCGTGGTAGATAACT 982
 Qy 121 ACGATACGGAGGCTTACCATCTGGCCCGAGTCTGCAATGATACCGGAAGCCACG 180
 Db 981 ACGATACGGAGGCTTACCATCTGGCCCGAGTCTGCAATGATACCGGAAGCCACG 923
 Qy 181 CTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCGGCGCAGCAGAAG 240
 Db 922 CTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCGGCGCAGCAGAAG 863
 Qy 241 TGGTCTGCAACTTATCCGCTCCATCCAGTCTTAATGTTGCGGGAAGCTAGAGT 300
 Db 862 TGGTCTGCAACTTATCCGCTCCATCCAGTCTTAATGTTGCGGGAAGCTAGAGT 803
 Qy 301 AAGTAGTTCGCGAGTAAATAGTTGGCAACGTTGTCATGCTCGAGGCAATCGTGT 360
 Db 802 AAGTAGTTCGCGAGTAAATAGTTGGCAACGTTGTCATGCTCGAGGCAATCGTGT 743
 Qy 361 GTCACGCTCGTGGTGGTAGGCTTCATTCAGTCCGTTCCCAAGCATCAAGCGAGT 420
 Db 742 GTCACGCTCGTGGTGGTAGGCTTCATTCAGTCCGTTCCCAAGCATCAAGCGAGT 683
 Qy 421 TACATGATCCCCATGTTGGCAAAAGCGTTAGTCTCTCGGTCCTCCGATCCTTGT 480
 Db 682 TACATGATCCCCATGTTGGCAAAAGCGTTAGTCTCTCGGTCCTCCGATCCTTGT 623
 Qy 481 CAGAAGTAAGTTGGCGCAG 500
 Db 622 CAGAAGTAAGTTGGCGCAG 603

RESULT 15
 AAK69629/c
 ID AAK69629 standard; DNA; 2212 BP.
 XX
 AC AAK69629;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24441.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001354.
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 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
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PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
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 PR 07-JUN-2000; 2000US-0209467P.
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 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
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 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
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 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
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 PR 29-SEP-2000; 2000US-0236369P.
 PR 02-OCT-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.

CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to prevent. CC protein. (I) proteins and polynucleotides may be used to prevent. CC diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC to AAK87694 represent human immune/haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169 CC represent sequences used in the exemplification of the present invention XX

SQ Sequence 2212 BP; 558 A; 537 C; 557 G; 560 T; 0 U; 0 Other;

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Best Local Similarity 99.2%; Pred. NO. 6.6e-112;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

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DB 1098 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTACGAGCACCTATCTCA 1039

QY 61 GCGATCTGTCTATTTCGTTTCATCCCATAGTGTGCTGCAACTCCCGCTCGTGTAGATAACT 120
DB 1038 GCGATCTGTCTATTTCGTTTCAT-CCATAGTGTGCTG-ACTCCCGCTCGTGTAGATAACT 982

QY 121 ACGATACGGGAGGGCTTACCATCTGCCCCAGTGTGCTGCAATGATACCGGAAGACCCACG 180
DB 981 ACGATACGGGAGGGCTTACCATCTGCCCCAGTGTGCTGCAATGATACCGG-AGACCCACG 923

QY 181 CTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCGCGGAGGCGGAGCGCAGAG 240
DB 922 CTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCGCGGAGGCGGAGCGCAGAG 863

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DB 862 TGGTCTCGCAACTTTATCCGCTCCATCCAGTCTATTATTTGTCGGGAAAGCTAGAGT 803

QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCATTTGTCAGGCAATCGTGTG 360
DB 802 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCATTTGTCAGGCAATCGTGTG 743

QY 361 GTCACGCTCGTGTGGTATGCTTCAATTCAGCTCCGCTTCCCAACGATCAAGGCGAGT 420
DB 742 GTCACGCTCGTGTGGTATGCTTCAATTCAGCTCCGCTTCCCAACGATCAAGGCGAGT 693

QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTTCCGCTCCTCCGATCGTTGT 480
DB 682 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTTCCGCTCCTCCGATCGTTGT 623

QY 481 CAGAAGTAAGTTGGCGCGAG 500
DB 622 CAGAAGTAAGTTGGCGCGAG 603

Search completed: April 29, 2005, 04:31:45
Job time : 441 secs

PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241826P.
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PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
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PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
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PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249214P.
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PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 03-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI . Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX - useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 24441; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 02:02:08 ; Search time 2527 Seconds
(without alignments)
7531.514 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	460.4	92.1	758	9	CL422788 AE0544 Sa
2	460.4	92.1	832	4	BG923768 602825893
C 3	459.4	91.9	635	1	AV610355 AV610355
C 4	449.4	89.9	523	1	AV610857 AV610857
C 5	446.8	89.4	854	4	BM438950 Iplvr0049
C 6	445.8	89.2	659	6	CD240106 DTL3P2A4
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. 19	388.4	77.7	855	4	BI664231 603289174
- 20	388.4	77.7	888	4	BI684711 603307057
21	386.8	77.4	911	4	BG923556 602823195
22	385.8	77.2	919	4	BI688972 603313450
23	381.4	76.3	477	1	AV605606 AV605606
24	377.8	75.6	872	4	BI855537 603382628

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ALIGNMENTS

CL422788 758 bp mRNA linear GSS 11-MAR-2004
AE0544 Sanger Institute Gene Trap Library pGT01xr Mus musculus
cdna, mRNA sequence.
CL422788
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GSS.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 758)
Sanger Institute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2003)
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES

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Matches 495; Conservative 0; Mismatches 1; Indels 4; Gaps 3;
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Db 201 ATATATGAGTAAACTTGGTCTGACAGTACCAATGCTTAATCAGTGAGGCACCTATCTCA 260
Qy 61 GCATCTGCTATTTCGTTTCATCCCATAGTTCGCTGCAACTCCCGTCGTTAGATAACT 120
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QY 181 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCCGCGGAGGCGGAGGAG 240
Db 377 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCCGCGGAGGCGGAGGAG 436
QY 241 TGGTCTCTGCAACTTTATTCGCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT 300
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QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGCTCCTCGGTCTCCGATCGTTGT 480
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ACCESSION BG923768
VERSION BG923768.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 832)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: gqapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
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High quality sequence stop: 823.
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Best Local Similarity 99.0%; Pred. No. 8e-139;
Matches 495; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

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QY 481 CAGAAGTAAGTTGGCCGCGAG 500
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DEFINITION mRNA sequence.
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VERSION AV610355.1 GI:9746025
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 635)
Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cdna libraries and determination of 36,000
bovine ESTs
Nucleic Acids Res. 29 (22), E108 (2001)
21570554
11713328
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725

```

Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

Email: kazuugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES

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was deleted from a NotI site"

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DEFINITION mRNA sequence.

ACCESSION AV610857
VERSION AV610857.1 GI:9746527
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SOURCE Bos taurus (cow)
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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE

1 (bases 1 to 523)
Takauega,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.

TITLE

and Sugimoto,Y.
Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs

JOURNAL

Nucleic Acids Res. 29 (22), E108 (2001)

MEDLINE

21570554

COMMENT

11713328
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazuugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES

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was deleted from a NotI site"

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DB 270 TGGTCTCTGCAACTTTATTCGCGCTCCATCCAGTCTATTAAATTTGTCGGGGAAGCTAGAGT 211
QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCGATGTCGATGTCGAGGCATCGTGT 360
DB 210 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCGATGTCGATGTCGAGGCATCGTGT 151
QY 361 GTACGCTCGTCTGTTGTTGATGCTTCAATCAGTCCGCTTCCCAACGATCAAGGCGAGT 420
DB 150 GTACGCTCGTCTGTTGTTGATGCTTCAATCAGTCCGCTTCCCAACGATCAAGGCGAGT 91
QY 421 TACATGATCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGCTCCTCCGATC-GTTG 479
DB 90 TACATGATCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGCTCCTCCGATCGTGT 31
QY 480 TCAGAAAGTAAGTTGGCCGCGAG 500
DB 30 TCAGAAAGTAAGTTGGCCGCGAG 10

RESULT 5

BM438950/c

LOCUS
 DEFINITION Bm438950 854 bp mRNA linear EST 31-JAN-2002
 Iplvr00491 Liver cDNA library Ictalurus punctatus cDNA 5', mRNA
 sequence.
 ACCESSION Bm438950
 VERSION Bm438950.1 GI:18460672
 KEYWORDS EST.
 SOURCE Ictalurus punctatus (channel catfish)
 ORGANISM Ictalurus punctatus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 Ictaluridae; Ictalurus.
 1 (bases 1 to 854)
 REFERENCE Peng,J., Kucukas,H., Kocabas,A., Li,P. and Liu,Z.
 Transcription of channel catfish (Ictalurus punctatus): initial
 analysis of expressed sequence tags from the liver
 Unpublished (2002)
 JOURNAL Contact: Liu ZJ
 COMMENT The Fish Molecular Genetics and Biotechnology Laboratory,
 Department of Fisheries and Allied Aquacultures and Program of Cell
 and Molecular Biosciences
 Auburn University
 203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
 Tel: 334 844 4054
 Fax: 334 844 9208
 Email: zliu@acesag.auburn.edu
 Seq primer: M13 Reverse.
 FEATURES
 source
 1..854
 Location/Qualifiers
 /organism="Ictalurus punctatus"
 /mol_type="mRNA"
 /db_xref="taxon:7998"
 /clone_lib="liver cDNA library"
 /note="Organ: Liver; Vector: pSport1; Site_1: NotI;
 Site_2: SalI"

ORIGIN

Query Match 89.4%; Score 446.8; DB 4; Length 854;
 Best Local Similarity 98.6%; Pred. No. 2.3e-134;
 Matches 493; Conservative 0; Mismatches 2; Indels 5; Gaps 4;
 QY 1 ATATATGAGTAACTTGGTCTGACAGTGA CCAATGCTTAATCATGAGGACCTATCTCA 60
 DB 842 ATATATGAGTAACTTGGTCTGACAGTGA CCAATGCTTAATCATGAGGACCTATCTCA 783
 QY 61 GCGATCTGTCTATTTCGTTCTATCCATAGTTCCTGCAACTCCCGTCGTGTAGATAACT 120
 DB 782 GCGATCTGTCTATTTCGTTCTATCCATAGTTCCTGCAACTCCCGTCGTGTAGATAACT 726
 QY 121 ACGATACGGAGGGCTTACCAATCTGGCCCAAGTCTGCAATGATACCGCGAAGACCCACG 180
 DB 725 ACGATACGGAGGGCTTACCAATCTGGCCCAAGTCTGCAATGATACCGCG-AGACCCACG 667
 QY 181 CTCACCGGCTCCAGATTATCAGCAATTAACACGACCGCGGAGGCGCGAGCGAGAG 240
 DB 666 CTCACCGGCTCCAGATTATCAGCAATTAACACGACCGCGGAGGCGCGAGCGAGAG 607
 QY 241 TGGTCTCGCACTTATTCGCTCCATCCAGTCTATTAATTGTTGCGGGAAGCTAGAGT 300
 DB 606 TGGTCTCGCACTTATTCGCTCCATCCAGTCTATTAATTGTTGCGGGAAGCTAGAGT 547
 QY 301 AAGTAGTTCGCGAGTAAATAGTTTTCGCAAGCTGTTGTTGCCATTGCTCGAGCATCGTGGT 360
 DB 546 AAGTAGTTCGCGAGTAAATAGTTTTCGCAAGCTGTTGTTGCCATTGCTCGAGCATCGTGGT 487
 QY 361 GTCACGCTCGCTGTTTGGTATAGGCTTCATTGAGTTCGCTCGGTTCCCAACGATCAAGCGGAGT 420
 DB 486 GTCACGCTCGCTGTTTGGTATAGGCTTCATTGAGTTCGCTCGGTTCCCAACGATCAAGCGGAGT 427
 QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTTCCTTCGGTCTCTCCGATCGTTGT 480
 DB 426 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCT-CTTCGGTCTCTCCGATCGTTGT 368
 QY 481 CAGAGTAGTAAGTTGGCCGCGAG 500

DB 367 CAGAGTAGTAAGTTGGCCGCGAG 348
 RESULT 6
 LOCUS CD240106 659 bp mRNA linear EST 14-APR-2004
 DEFINITION DT13P2M4 THP-1 OligodT Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD240106
 VERSION CD240106.1 GI:38044974
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 659)
 REFERENCE Khabar,K.S., Dhalla,M., Al-Haj,L., Bakheet,T., Sy,C. and
 Naemuddin,M.
 Selection of AU-rich transiently expressed sequences: reversal of
 CDNA abundance
 JOURNAL RNA 10 (4), 747-753 (2004)
 COMMENT Contact: Khalid S.A Khabar
 Interferons and Cytokines Unit
 King Faisal Specialist Hospital and Research Centre
 P.O. Box 3354, MBC-03, RIYADH 11211, Saudi Arabia
 Tel: 966-1-442-7876
 Fax: 966-1-442-7858
 Email: khabar@kfshrc.edu.sa.
 FEATURES
 source
 1..659
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_type="Monocytes"
 /cell_line="THP-1"
 /clone_lib="THP-1 OligodT Library"
 /note="Vector: PT7BLUE2 blunt cloning vector (Novagen);
 Site 1: SmaI; Site 2: SmaI; The library was prepared from
 LPS-stimulated cell line pre-treated with cycloheximide."

ORIGIN

Query Match 89.2%; Score 445.8; DB 6; Length 659;
 Best Local Similarity 98.8%; Pred. No. 4.5e-134;
 Matches 481; Conservative 0; Mismatches 2; Indels 4; Gaps 3;
 QY 14 CTTTGGTCTCAGAGTTACCAATGCTTAATCAGTGAGGACCTATCTCAGCGATCTGTCTAT 73
 DB 46 CTTTGGTCTCAGAGTTACCAATGCTTAATCAGTGAGGACCTATCTCAGCGATCTGTCTAT 105
 QY 74 TTCTGTTTCATCCATAGTTGCTTGCCTGCAACTCCCGTCTGTGTAGATAACTACGATACGGGAGG 133
 DB 106 TTCTGTTTCAT-CCATAGTTGCTTGCCTG--ACTCCCGTCTGTGTAGATAACTACGATACGGGAGG 162
 QY 134 GCTTACCATCTGCGCCCAAGTCTGCAATCATACCGGAGAGCCACGCTCACCGGCTCCA 193
 DB 163 GCTTACCATCTGCGCCCAAGTCTGCAATCATACCGG-AGACCCAGCTCACCGGCTCCA 221
 QY 194 GATTATCAGCAATAAACCCAGCCAGCCGGAAGGCGGAGCGAGAGTGGTCTGCAACT 253
 DB 222 GATTATCAGCAATAAACCCAGCCAGCCGGAAGGCGGAGCGAGAGTGGTCTGCAACT 281
 QY 254 TTATCCGCTTCCATCCAGTCTATTAAATTGTTGCGGGAAGCTAGAGTAAGTAGTTCGCCA 313
 DB 282 TTATCCGCTTCCATCCAGTCTATTAAATTGTTGCGGGAAGCTAGAGTAAGTAGTTCGCCA 341
 QY 314 GTTAATAGTTTTCGCAACGTTGTTGCCATTGCTGAGGCAATCGTGGTGTCAAGCTCTGTG 373
 DB 342 GTTAATAGTTTTCGCAACGTTGTTGCCATTGCTGAGGCAATCGTGGTGTCAAGCTCTGTG 401
 QY 374 TTTGGTATGCTTCAATTCAGCTCCCGGTTCCCAACGATCAAGCGGAGTTACATGATCCCC 433
 DB 402 TTTGGTATGCTTCAATTCAGCTCCCGGTTCCCAACGATCAAGCGGAGTTACATGATCCCC 461

QY 434 ATGTTGTCAGAAAGCGGTAGTCTCGGTCTCGGATCGTGTGTCAGAGTAAGTTG 493
 Db 462 ATGTTGTCAGAAAGCGGTAGTCTCGGTCTCGGATCGTGTGTCAGAGTAAGTTG 521
 QY 494 GCGCAG 500
 Db 522 GCGCAG 528

RESULT 7
 BJ695105
 LOCUS
 DEFINITION BJ695105 HREST library Haplochromis sp. 'red tail sheller' CDNA
 clone nos75f01, mRNA sequence.
 ACCESSION BJ695105
 VERSION BJ695105.1 GI:46538226
 KEYWORDS
 SOURCE Haplochromis sp. 'red tail sheller'
 ORGANISM Haplochromis sp. 'red tail sheller',
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorphi; Acanthopterygii; Percomorpha; Perciformes;
 Labroidae; Cichlidae; Haplochromis.
 REFERENCE 1 (bases 1 to 626)
 Watanabe,M., Kobayashi,N., Shin-i,T., Kohara,Y. and Okada,N.
 Oxf sequences of cichlid in Lake Victoria are essentially same
 Unpublished (2004)
 JOURNAL Tadasu Shin-i
 COMMENT Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES
 source
 1..626
 /organism="Haplochromis sp. 'red tail sheller'"
 /mol_type="mRNA"
 /db_xref="taxon:257976"
 /clone="no575f01"
 /issue_type="jav"
 /dev_stage="varied"
 /clone_lib="HREST library"

ORIGIN
 Query Match 88.9%; Score 444.4; DB 4; Length 626;
 Best Local Similarity 99.0%; Pred. No. 1.3e-133;
 Matches 479; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

QY 17 GGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGCTATTTC 76
 Db 1 GGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGCTATTTC 60
 QY 77 GTTATCCCATAGTGTGCTCACTCCCTCGTGTAGATAGTACGATACGGAGGGCT 136
 Db 61 GTTTCAT-CCATAGTGTGCTG--ACTCCCTCGTGTAGATAGTACGATACGGAGGGCT 117
 QY 137 TACCATCTGCCCCAGTGTGCAATGATACCGCGAGACCCAGCTCAGCGCTCCAGAT 196
 Db 118 TACCATCTGCCCCAGTGTGCAATGATACCGCG-AGACCCAGCTCAGCGCTCCAGAT 176
 QY 197 TTATCAGCAATAACACGACGCGGAGGCGGAGAGTGTCTGCAACTTTA 256
 Db 177 TTATCAGCAATAACACGACGCGGAGGCGGAGAGTGTCTGCAACTTTA 236
 QY 257 TCGCCCTCCATCCAGTCTATTATTTGTTGCGGGAAGCTAGATAGTTCGCCAGTT 316
 Db 237 TCGCCCTCCATCCAGTCTATTATTTGTTGCGGGAAGCTAGATAGTTCGCCAGTT 296
 QY 317 AATAGTTTGGCAACGTTGTTGCAATGCTGCAAGGATCGTGTGTCAGCTCGTGT 376
 Db 297 AATAGTTTGGCAACGTTGTTGCAATGCTGCAAGGATCGTGTGTCAGCTCGTGT 356

QY 377 GGTATGCTTCATTTCAGTCCGTTCCCAACGATCAAGGCGAGTTACATATCCCCCATG 436
 Db 357 GGTATGCTTCATTTCAGTCCGTTCCCAACGATCAAGGCGAGTTACATATCCCCCATG 416
 QY 437 TTGTGCAAAAAGCGGTTAGTCTCTTCGGTCTCCGATCGTGTGCAAGAAGTAAGTTGCC 496
 Db 417 TTGTGCAAAAAGCGGTTAGTCTCTTCGGTCTCCGATCGTGTGCAAGAAGTAAGTTGCC 476
 QY 497 GCAG 500
 Db 477 GCAG 480

RESULT 8
 AG011001/c
 LOCUS
 DEFINITION AG011001 Homo sapiens genomic DNA, 21q region, clone: 879G12X91, genomic survey sequence.
 ACCESSION AG011001 AG004662
 VERSION AG011001.1 GI:3357935
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 721)
 Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
 TITLE Homo sapiens genomic DNA, chromosome 21q
 JOURNAL Published Only in DataBase (1998)
 REFERENCE 2 (bases 1 to 721)
 Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL
 COMMENT On Feb 5, 1999 this sequence version replaced gi:2826191.
 AG004662: Submitted (30-Jan-1998).

FEATURES
 Location/Qualifiers
 1..721
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="21"
 /map="21q"
 /clone="879G12X91"

ORIGIN
 Query Match 88.5%; Score 442.4; DB 9; Length 721;
 Best Local Similarity 98.8%; Pred. No. 5.9e-133;
 Matches 488; Conservative 0; Mismatches 1; Indels 5; Gaps 4;

QY 7 GAGTAACTTGCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATC 66
 Db 584 GAGTAACTTGCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATC 536
 QY 67 TGCTATTTTGGTTCATCCCATAGTTGCTGCAACTCCCGTCTGTAGATAACTACGATA 126
 Db 525 TGCTATTTTGGTTCAT-CCATAGTTGCTG--ACTCCCGTCTGTAGATAACTACGATA 469
 QY 127 CGGAGGGGTTTACCACTCTGCCCCAGTGTGCAATGATACCGCGAAGACCCAGCTCACC 186
 Db 468 CGGAGGGGTTTACCACTCTGCCCCAGTGTGCAATGATACCGCG-AGACCCAGCTCACC 410
 QY 187 GGTTCAGATTTTATCAGCAATAAACACGACGCGGAGGCGGAGAGTGTGCTCC 246
 Db 409 GGTTCAGATTTTATCAGCAATAAACACGACGCGGAGGCGGAGAGTGTGCTCC 350
 QY 247 TGCACCTTTTATCGGCTCCATCCAGTCTATTATTTGTTGCGGGAAGCTAGAGTAAGTAG 306
 Db 349 TGCACCTTTTATCGGCTCCATCCAGTCTATTATTTGTTGCGGGAAGCTAGAGTAAGTAG 290
 QY 307 TTGCCAGTTAATAGTGTTCGCAACGTTGTTGCTTGTGCGGATCGTGTGTCACG 366

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Db      289  TTCCGAGTTAAATAGTTTGGCGAAGTTGTTGCCATTGCTACAGGCATGCTGGTGTCAAG 230
QY      367  CTGCTGGTTGGTATGGCTTCATTACAGTCCGGTTCCTCCCAACGATCAAGCGAGTTACATG 426
Db      229  CTGCTGGTTGGTATGGCTTCATTACAGTCCGGTTCCTCCCAACGATCAAGCGAGTTACATG 170
QY      427  ATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTCTCAGAAG 486
Db      169  ATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTCTCAGAAG 110
QY      487  TAAAGTTGGCCGCGAG 500
Db      109  TAAAGTTGGCCGCGAG 96

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RESULT 9
AG014394
LOCUS   Homo sapiens genomic DNA, 21q region, clone: B355C24SpN18, genomic
DEFINITION survey sequence.
ACCESSION AG014394
VERSION   AG014394.1 GI:3608292
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens

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REFERENCE
AUTHORS  Hattori.N., Ishii.K., Toyoda.A., Shiba.T. and Sakaki.Y.
TITLE    Homo sapiens genomic DNA, chromosome 21q
JOURNAL  Published Only in DataBase (1998)
REFERENCE
AUTHORS  Hattori.N., Ishii.K., Toyoda.A., Shiba.T. and Sakaki.Y.
TITLE    Direct Submission
JOURNAL  Submitted (17-SEP-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgsc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)

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1. .689
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="B355C24SpN18"

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ORIGIN
Query Match      87.8%; Score 438.8; DB 9; Length 689;
Best Local Similarity 98.8%; Pred. No. 8.7e-132;
Matches 474; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY      17  GGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCACTATCTCAGGAGCTGCTATTTC 76
Db      30  GGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCACTATCTCAGGAGCTGCTATTTC 89
QY      77  GTTCATCCCATAGTTGGCTGCAACTCCCGTGTGTAGATAACTACGATACGGAGGGCT 136
Db      90  GTTCAT-CCATAGTTGGCTG- -ACTCCCGTGTGTAGATAACTACGATACGGAGGGCT 146
QY      137  TACCATCTGCCCGCAGTGTGCAATGATACCGGAGAACCCAGCTCACCAGGCTCCAGAT 196
Db      147  TACCATCTGCCCGCAGTGTGCAATGATACCGG-AGACCCAGCTCACCAGGCTCCAGAT 205
QY      197  TTATCAGCAATAAACACGAGCCGAGGAGGCGGAGCGAGCAAGTGGTCTCTGCAACTTTA 256
Db      206  TTATCAGCAATAAACACGAGCCGAGGAGGCGGAGCGAGCAAGTGGTCTCTGCAACTTTA 265
QY      257  TCGCCTCCATCCAGTCTATTATTGTTGCGGGAAGCTAGTAAAGTTCGCCAGTT 316
Db      266  TCGCCTCCATCCAGTCTATTATTGTTGCGGGAAGCTAGTAAAGTTCGCCAGTT 325

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QY      317  AATAGTTTCGCAACGTTGTTGCCATTGCTGCAGGCATGCTGGTGTACGCTCGTCGTTT 376
Db      326  AATAGTTTCGCAACGTTGTTGCCATTGCTGCAGGCATGCTGGTGTACGCTCGTCGTTT 385
QY      377  GGTATGGCTTCATTACAGTCCGGTTCCTCCCAACGATCAAGCGAGTTACATGATCCCCCATG 436
Db      386  GGTATGGCTTCATTACAGTCCGGTTCCTCCCAACGATCAAGCGAGTTACATGATCCCCCATG 445
QY      437  TTGTGCAAAAGGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGTGAGAAGTAAAGTTGGCC 496
Db      446  TTGTGCAAAAGGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGTGAGAAGTAAAGTTGGCC 505

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RESULT 10
BM438846/c
LOCUS   BM438846
DEFINITION Iplvr00157 Liver cdna library Ictalurus punctatus cdna 5', mRNA
sequence.
ACCESSION BM438846
VERSION   BM438846.1 GI:18460568
KEYWORDS  EST.
SOURCE    Ictalurus punctatus (channel catfish)
ORGANISM  Ictalurus punctatus

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REFERENCE
AUTHORS  Feng,J., Kucuktas,H., Kocabas,A., Li,P. and Liu,Z.
TITLE    Transcriptome of channel catfish (Ictalurus punctatus): initial
analysis of expressed sequence tags from the liver
JOURNAL  Unpublished (2002)
COMMENT  Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
Location/Qualifiers
1. .1013
/organism="Ictalurus punctatus"
/mol_type="mRNA"
/db_xref="taxon:7998"
/clone_lib="Liver cdna library"
/note="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: SalI"

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1. .1013
/organism="Ictalurus punctatus"
/mol_type="mRNA"
/db_xref="taxon:7998"
/clone_lib="Liver cdna library"
/note="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: SalI"

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ORIGIN
Query Match      87.5%; Score 437.4; DB 4; Length 1013;
Best Local Similarity 98.6%; Pred. No. 2.8e-131;
Matches 494; Conservative 0; Mismatches 1; Indels 6; Gaps 5;

QY      1  ATATATGAGTAAACCTTGGTCTGCACAGTTACCAATGCTTAATCAGTGAGGACCACTATCTCA 60
Db      842  ATATATGAGTAAACCTTGGTCTGCACAGTTACCAATGCTTAATCAGTGAGGACCACTATCTCA 783
QY      61  GCGATCTGTCTATTGTTTCATCCCATAGTTGGCTGCAACTCCCGTGTGTAGATAACT 120
Db      782  GCGATCTGTCTATTGTTTCAT-CCATAGTTGCTG- -ACTCCCGTGTGTAGATAACT 726
QY      121  ACGATACGGAGGGCTTACCATCTGCCCGCAGTGTGCAATGATACCGGAGACCCACG 180
Db      725  ACGATACGGAGGGCTTACCATCTGCCCGCAGTGTGCAATGATACCGG-AGACCCACG 667
QY      181  CTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCGGAGGCGGAGCGCAAG 240
Db      666  CTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCGGAGGCGGAGCGCAAG 607
QY      241  TGGTCTCTGCAACTTTATTCGCGCTCCATCCAGTCTATTATTGTTGCGGGAAGCTAGAGT 300

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Db      606 TGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAGCTAGAGT 547
Qy      301 AAGTAGTCCCAAGTTAATAGTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT 360
Db      546 AAGTAGTTCGCCAGTTAATAGTTTGGCAACAGTTGTTGCCATTGCTACAGGCATCGTGGT 487
Qy      361 GTCACGCTCGCTGTTGGTATGGCTTCATTTCAGCTCCGGTTCCTCCACGATCAAGCGAGT 420
Db      486 GTCACGCTCGCTGTTGGTATGGCTTCATTTCAGCTCCGGTTCCTCCACGATCAAGCGAGT 427
Qy      421 TACA-TGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCTCGGTCCTCCGATCGTTG 479
Db      426 TACATTGATCCCCCATGTTGTGCAAAAAGCGGTTAGCT-CTTCGGTCTCCGATCGTTG 368
Qy      480 TCAGAACTAGTTGGCCGAG 500
Db      367 TCAGAACTAGTTGGCCGAG 347

RESULT 11
AG009976/c
LOCUS      Homo sapiens genomic DNA, 21q region, clone: T485XN, genomic survey
DEFINITION
ACCESSION      AG003787
VERSION        AG009976.1 GI:3289962
KEYWORDS      GSS.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          Hattori.M., Ishii.K., Toyoda.A., Shiba.T. and Sakaki.Y.
JOURNAL        Published Only in DataBase (1998)
REFERENCE      2 (bases 1 to 698)
AUTHORS        Hattori.M., Ishii.K., Toyoda.A., Shiba.T. and Sakaki.Y.
TITLE          Direct Submission
JOURNAL        Submitted (06-JUL-1998) Masahira Hattori, Kitasato University,
COMMENT        Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
                Sagamihara 228 Japan (E-mail:hattori@hc.ims.u-tokyo.ac.jp,
                Tel:0427-78-9732, Fax:0427-78-9561)
                On Feb 5, 1999 this sequence version replaced gi:2754689.
                AG003787: Submitted (07-Jan-1998).
FEATURES             Location/Qualifiers
     source          1..698
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q"
                     /clone="T485XN"

ORIGIN
Query Match      87.3%; Score 436.6; DB 9; Length 698;
Best Local Similarity 98.0%; Pred. No. 4.6e-131;
Matches 485; Conservative 0; Mismatches 4; Indels 6; Gaps 4;

Qy      7  GAGTAACTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCAGCG-AT 65
Db      581 GAGTAACTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCAGCGAAT 522
Qy      66  CTGCTATTTCGTTTCATCCCATAGTTCCTGCAACTCCCGTCTGTAGATACTACGAT 125
Db      521 CTGCTATTTCGTTTCAT-CCATAGTTGCCTG---ACTCCGCTGTGTAGATACTACGAT 466
Qy      126 ACGGGAGGGCTTACCATCTCGCCCGAGTGTGCAATGATACCGGAGAACCCAGCTCAC 185
Db      465 ACGGGAGGGCTTACCATCTCGCCCGAGTGTGCAATGATACCGCG-AGACCCAGCTCAC 407
Qy      186 CGGCTCCAGTTTATTCAGCAATAAACAGCAGCCGAGGAGGCGGAGGAGTGGTC 245
Db      406 CGGCTCCAGTTTATCAGCAATAAACAGCAGCCGAGGAGGCGGAGGAGTGGTC 347

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Qy      246 CTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAGCTAGAGTAA 305
Db      346 CTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAGCTAGAGTAA 287
Qy      306 GTTCGCCAGTTAATAGTTTGGCAACAGTTGTTGCCATTCTGTCAGGCATCGTGGTCTAC 365
Db      286 GTTCGCCAGTTAATAGTTTGGCAACAGTTGTTGCCATTCTGTCAGGCATCGTGGTCTAC 227
Qy      366 GCTCGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 425
Db      226 GCTCGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 167
Qy      426 GATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCTCGGTCCTCCGATCGTTGTCAGAA 485
Db      166 GATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCTCGGTCCTCCGATCGTTGTCAGAA 107
Qy      486 GTAAGTTGGCCGAG 500
Db      106 GTAAGTTGGCCGAG 92

RESULT 12
CD649375/c
LOCUS      Crassostrea virginica Gonad Crassostrea virginica cDNA
DEFINITION
ACCESSION      CD649375
VERSION        CD649375.1 GI:31906346
KEYWORDS      EST.
SOURCE        Crassostrea virginica (eastern oyster)
ORGANISM      Crassostrea virginica
REFERENCE      Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
AUTHORS        Ostreidae; Crassostrea.
TITLE          1 (bases 1 to 819)
JOURNAL        Peatman,E., Kucuktas,H., Li,P., He,C., Feng,J., Wei,X. and Liu,Z.
COMMENT        Differentially expressed oyster (Crassostrea virginica) genes after
                exposure to mercury
                Contact: Liu ZJ
                The Fish Molecular Genetics and Biotechnology Laboratory,
                Department of Fisheries and Allied Aquacultures and Program of Cell
                and Molecular Biosciences
                Auburn University
                203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
                Tel: 334 844 4054
                Fax: 334 844 9208
                Email: zliu@acesag.auburn.edu
                Seq primer: M13 Reverse.
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                     /note="Organ: Gonad; Vector: pSport1; Site_1: NotI;
                     Site_2: SalI"

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Best Local Similarity 98.7%; Pred. No. 1e-127;
Matches 472; Conservative 0; Mismatches 1; Indels 5; Gaps 4;

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Qy      83  CCCATAGTTGCTGCAACTCCCGTGTGTAGATACTACGATACGGAGGGGTTACCAT 142
Db      759 -CCATAGTTGCTG--ACTCCCGTGTGTAGATACTACGATACGGAGGGGTTACCAT 703
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/notes="vector: pZL1; Site 1: SalI; Site 2: NotI; Poly A
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Matches 432; Conservative 0; Mismatches 5; Indels 4; Gaps 3;

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DB 234 GCGATCTGCTATTTCCTCAT--CCATAGTTGCTG--ACTCCCGCTGCTGTAGATAACT 290
QY 121 ACGATCGGAGGGCTTACCATCTGGCCCGCAGTCTGCTCAATGATACCGCGAAGCCACG 180
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QY 181 CTCACGGCTCCAGATTATCAGCAATAAACACGAGCCGCGAAGGCCGAGCGCAGAAG 240
DB 350 CTCACGGCTCCAGATTATCAGCAATAAACACGAGCCGCGAAGGCCGAGCGCAGAAG 409
QY 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTTATTAATTTGTCGCGGAAGCTAGAGT 300
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QY 361 GTACGCTCTGCTGTTGGTAGTCTCATTCAGTCCGCTTCCCAACGATCAAGGCGAGT 420
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RESULT 15
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DEFINITION NF018A07IRf1052 Irradiated Medicago truncatula cDNA clone
SOURCE     NF018A07IR 5', mRNA sequence.
ACCESSION  BQ152411
VERSION    BQ152411.1 GI:20289470
KEYWORDS   EST.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
            1 (bases 1 to 796)
REFERENCE  Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
            Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula irradiated library
            Unpublished (2001)
            Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 224 6650
            Fax: 580 224 6692
            Email: gdmay@noble.org
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FEATURES
source

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/notes="Vector: Lambda Zap; Seedlings were exposed either
to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the E. coli strain XL1-Blue MRP'
(Stratagene). Excised plasmids were plated using SOLR
cells."
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ORIGIN

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Query Match      79.4%; Score 396.8; DB 5; Length 796;
Best Local Similarity 89.0%; Pred. No. 4.9e-118;
Matches 443; Conservative 0; Mismatches 50; Indels 5; Gaps 4;

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QY 61 GCGATCTGCTATTTCCTCATCCCATAGTTGCTGCAACTCCCGCTGCTGTAGATAACT 120
DB 287 GCGATCTGCTATTTCCTCAT--CCATAGTTGCTG--ACTCCCGCTGCTGTANATAACT 343
QY 121 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAAGACCCACG 180
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QY 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTTATTAATTTGTCGCGGAAGCTAGAGT 300
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QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTCAGGCAATCGTGGT 360
DB 523 AANTANTTCCNCANTTTAATANTTTGGCAACNTTTGTCATTTGCTACANGCATCNTGGT 582
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QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTAGTCTCTTCGGTCTCCGATCTGTTGT 480
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QY 481 CAGAAGTAAGTTGGCGCG 498
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	462	92.4	1905	1	US-08-594-469-9
2	462	92.4	1905	2	US-08-906-957-9
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4	462	92.4	3003	6	5182260-18
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6	462	92.4	3122	3	US-09-042-353-152
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8	462	92.4	3418	2	US-08-944-916-12
9	462	92.4	3516	3	US-09-058-483-9
10	462	92.4	3656	1	US-08-232-463-8
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22	462	92.4	3754	4	US-08-379-611-17
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25	462	92.4	3803	1	US-07-640-476-1
26	462	92.4	3878	3	US-08-651-472-65
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28	462	92.4	4023	4	US-08-809-513A-8	Sequence 8, Appli
29	462	92.4	4366	4	US-08-586-740A-12	Sequence 12, Appli
30	462	92.4	4378	4	US-08-586-740A-9	Sequence 9, Appli
31	462	92.4	4410	1	US-08-594-469-1	Sequence 1, Appli
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34	462	92.4	4557	4	US-08-778-717-5	Sequence 5, Appli
35	462	92.4	4659	1	US-08-232-463-10	Sequence 10, Appli
36	462	92.4	4701	3	US-08-651-472-64	Sequence 64, Appli
37	462	92.4	4701	3	US-08-358-928-64	Sequence 64, Appli
38	462	92.4	4818	1	US-08-232-463-11	Sequence 11, Appli
39	462	92.4	4819	1	US-08-450-257-20	Sequence 20, Appli
40	462	92.4	4819	1	US-08-450-246-20	Sequence 20, Appli
41	462	92.4	4819	1	US-08-450-098-20	Sequence 20, Appli
42	462	92.4	4819	1	US-08-451-233-20	Sequence 20, Appli
43	462	92.4	4819	1	US-08-450-236-20	Sequence 20, Appli
44	462	92.4	4819	3	US-08-235-403-20	Sequence 20, Appli
45	462	92.4	4821	1	US-08-232-463-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-08-594-469-9
; Sequence 9, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOMBE, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1905 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-594-469-9

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Best Local Similarity 99.2%; Pred. No. 1.2e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

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; Sequence 9, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E

; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1905 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-9

Query Match 92.4%; Score 462; DB 2; Length 1905;
Best Local Similarity 99.2%; Pred. No. 1.2e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

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RESULT 3

US-09-202-904A-13/c
; Sequence 13, Application US/09202904A
; Patent No. 6395471
; GENERAL INFORMATION:
; APPLICANT: Kang, Sung Key
; APPLICANT: Hahn, Bumsuk
; TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing
; TITLE OF INVENTION: the Activity of Hepatitis C Virus Protease, a Recombinant
; TITLE OF INVENTION: Gene and a Use Thereof
; FILE REFERENCE: A32210-PCT-USA 072944.0104
; CURRENT APPLICATION NUMBER: US/09/202,904A
; FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/KR97/00120
; PRIOR FILING DATE: 1997-06-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13

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; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Genetically engineered virus derived from
; OTHER INFORMATION: poliovirus and hepatitis C virus
; US-09-202-904A-13

Query Match          92.4%; Score 462; DB 3; Length 2320;
Best Local Similarity 99.2%; Pred. No. 1.5e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

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Db 1506 ATATATGAGTAAACTTGGCTGACAGTTACCAATGCTTAATCAAGTGGGACCTATCTCA 1565

Qy 61 GCGATCTGTCTATTTTCGTTTCATCCCACTAGTGTGCTGCAACTCCCGTCCGTTAGATAA 120
    |||||
Db 1566 GCGATCTGTCTATTTTCGTTTCAT--CCATAGTTGCGTG--ACTCCCCGTGCTGTAGATAA 1622

Qy 121 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGG-AGACCCACG 180
    |||||
Db 1623 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGG-AGACCCACG 1681

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Qy 301 AAGTAGTTCCGCAAGTTAATAGTTTGGCAACGTTGTTGCCATTGCTGCGGCAATCGTGT 360
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Qy 481 CAGAAGTAAAGTTGGCCGCGAG 500
    |||||
Db 1982 CAGAAGTAAAGTTGGCCGCGAG 2001

RESULT 5
5182260-18
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:18:
; LENGTH: 3003
5182260-18

Query Match          92.4%; Score 462; DB 6; Length 3003;
Best Local Similarity 99.2%; Pred. No. 1.5e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

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Qy 61 GCGATCTGTCTATTTTCGTTTCATCCCACTAGTGTGCTGCAACTCCCGTCCGTTAGATAA 120
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Query Match          92.4%; Score 462; DB 6; Length 3003;
Best Local Similarity 99.2%; Pred. No. 1.5e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:18:
; LENGTH: 3003
5182260-18

Query Match          92.4%; Score 462; DB 6; Length 3003;
Best Local Similarity 99.2%; Pred. No. 1.5e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:18:
; LENGTH: 3003
5182260-18
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181	Qy	CTCACCGGCTCCAGATTATCAGCAATAAAACAGCCAGCCGGGAAGGGCCGAGCCGACAAG	240
1682	Db	CTCACCGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGGAAGGGCCGAGCCGACAAG	1741
241	Qy	TGGTCCTGCACAATTATCCGCCTCCATCCAGTCTATTAATTTGTCGCGGAAGCTAGAGT	300
1742	Db	TGGTCCTGCACAATTATCCGCCTCCATCCAGTCTATTAATTTGTCGCGGAAGCTAGAGT	1801
301	Qy	AAGTAGTTCCGCAGTTAATAGTTTGCACAAGTGTGGTGCATCTCGAGGCAATCGTGGT	360
1802	Db	AAGTAGTTCCGCAGTTAATAGTTTGCACAAGTGTGGTGCATCTCGAGGCAATCGTGGT	1861
361	Qy	GTACAGCTCGTGGTTGGTATGGCTTCATTACAGTCCGGTTCCCAACGATCAAGGCCAGT	420
1862	Db	GTACAGCTCGTGGTTGGTATGGCTTCATTACAGTCCGGTTCCCAACGATCAAGGCCAGT	1921
421	Qy	TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGT	480
1922	Db	TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGT	1981
481	Qy	CAGAAGTAAGTTGGCCGCAG	500
1982	Db	CAGAAGTAAGTTGGCCGCAG	2001

RESULT 6

US-09-042-353-152
 / Sequence 152, Application US/09042353
 / Patent No. 6255458
 / GENERAL INFORMATION:
 / APPLICANT: Lonberg, Nils
 / APPLICANT: Kay, Robert M.
 / TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
 / TITLE OF INVENTION: Producing Heterologous Antibodies
 / NUMBER OF SEQUENCES: 421
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Townsend and Townsend and Crew LLP
 / STREET: Two Embarcadero Center, Eighth Floor
 / CITY: San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94111-3834
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA: US/09/042,353
 / APPLICATION NUMBER: US/09/042,353
 / FILING DATE: 13-MAR-1998
 / CLASSIFICATION: 800
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/810,279
 / FILING DATE: 17-DEC-1991
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/853,408
 / FILING DATE: 18-MAR-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/904,068
 / FILING DATE: 23-JUN-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/990,860
 / FILING DATE: 16-DEC-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/053,131
 / FILING DATE: 26-APR-1993
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/096,762
 / FILING DATE: 22-JUL-1993
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/155,301
 / FILING DATE: 18-NOV-1993
 / PRIOR APPLICATION DATA:

Qy 421 TACATGATCCCAATGTTGTGCAAAAAAGCGGTAGCTCTCGGTCTCGATCGTTGT 480
 Db 2446 TACATGATCCCAATGTTGTGCAAAAAAGCGGTAGCTCTCGGTCTCGATCGTTGT 2505
 Qy 481 CAGAACTAAGTTGGCCGCGAG 500
 Db 2506 CAGAACTAAGTTGGCCGCGAG 2525

RESULT 7

US-08-758-417A-416
 ; Sequence 416, Application US/08/58417A
 ; Patent No. 6300129
 ; GENERAL INFORMATION:
 ; APPLICANT: Lonberg, Nils
 ; Kay, Robert M.
 ; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
 ; Producing Heterologous Antibodies
 ; NUMBER OF SEQUENCES: 417
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/758,417A
 ; FILING DATE: 02-Dec-1996
 ; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463
 FILING DATE: 10-OCT-1996
 APPLICATION NUMBER: US 08/544,404
 FILING DATE: 10-OCT-1995
 APPLICATION NUMBER: US 08/352,322
 FILING DATE: 07-DEC-1994
 APPLICATION NUMBER: US 08/209,741
 FILING DATE: 09-MAR-1994
 APPLICATION NUMBER: US 08/165,699
 FILING DATE: 10-DEC-1993
 APPLICATION NUMBER: US 08/161,739
 FILING DATE: 03-DEC-1993
 APPLICATION NUMBER: US 08/155,301
 FILING DATE: 18-NOV-1993
 APPLICATION NUMBER: US 08/096,762
 FILING DATE: 22-JUL-1993
 APPLICATION NUMBER: US 08/053,131
 FILING DATE: 26-APR-1993
 APPLICATION NUMBER: US 07/990,860
 FILING DATE: 16-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Serafini, Andrew T.
 REGISTRATION NUMBER: 41,303
 REFERENCE/DOCKET NUMBER: 014643-009030US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 416:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3122 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 * SEQUENCE DESCRIPTION: SEQ ID NO: 416:
 US-08-758-417A-416

Query Match 92.4%; Score 462; DB 3; Length 3122;
 Best Local Similarity 99.2%; Pred. No. 1.5e-150;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
 Qy 1 ATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
 Db 2030 ATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 2089
 Qy 61 GCATCTGTCTATTTCGTTTCATCCCATAGTTGCTGCAACTCCCGTCGTTGAGATAAAT 120
 Db 2090 GCATCTGTCTATTTCGTTTCATCCCATAGTTGCTGCAACTCCCGTCGTTGAGATAAAT 2146
 Qy 121 ACGATACGGAGGGCTTACCATCTGCCCCAGTGTGCAATGATACCGGAAAGACCCACG 180
 Db 2147 ACGATACGGAGGGCTTACCATCTGCCCCAGTGTGCAATGATACCGG-AGACCCACG 2205
 Qy 181 CTCACCGGCTCCAGATTATCAGCAATAACCCAGCCGCGGAGGCGGAGGCGAGNAG 240
 Db 2206 CTCACCGGCTCCAGATTATCAGCAATAACCCAGCCGCGGAGGCGGAGGCGAGNAG 2265
 Qy 241 TGGTCTCTGCAACTTTATCCGCTCCCATCCAGTCTAATTAATTTGTCGGGAAAGCTAGAGT 300
 Db 2266 TGGTCTCTGCAACTTTATCCGCTCCCATCCAGTCTAATTAATTTGTCGGGAAAGCTAGAGT 2325
 Qy 301 AAGTAGTTCCGCCAGTTAATAGTTTGGCAACAGTTTGGCCATTGCTGCAGGCAATCGTGT 360
 Db 2326 AAGTAGTTCCGCCAGTTAATAGTTTGGCAACAGTTTGGCCATTGCTGCAGGCAATCGTGT 2385
 Qy 361 GTCACGCTCGTGTGTTGGTATGCTTCATTCAGTCCGGTCCCAACGATCAAGGCGAGT 420
 Db 2386 GTCACGCTCGTGTGTTGGTATGCTTCATTCAGTCCGGTCCCAACGATCAAGGCGAGT 2445
 Qy 421 TACATGATCCCAATGTTGTGCAAAAAAGCGGTAGCTCTCGGTCTCCCGATCGTTGT 480
 Db 2446 TACATGATCCCAATGTTGTGCAAAAAAGCGGTAGCTCTCGGTCTCCCGATCGTTGT 2505
 Qy 481 CAGAACTAAGTTGGCCGCGAG 500
 Db 2506 CAGAACTAAGTTGGCCGCGAG 2525

RESULT 8

US-08-944-916-12
 ; Sequence 12, Application US/08944916
 ; Patent No. 5948622
 ; GENERAL INFORMATION:
 ; APPLICANT: Reznikoff, William S
 ; APPLICANT: Goryshin, Igor Y
 ; APPLICANT: York, Dona L
 ; APPLICANT: Zhou, Hong
 ; TITLE OF INVENTION: System for In Vitro Transposition
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Quarles & Brady
 ; STREET: 1 South Pinckney Street
 ; CITY: Madison
 ; STATE: WI
 ; COUNTRY: USA
 ; ZIP: 53703
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/944,916
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/814,877
 ; FILING DATE: 09-SEP-1996
 ; PRIOR APPLICATION DATA:

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1  APPLICATION NUMBER:  US 08/850,880
2  FILING DATE:  02-MAY-1997
3  ATTORNEY/AGENT INFORMATION:
4  NAME:  Berson, Bennett J
5  REGISTRATION NUMBER:  37094
6  REFERENCE/DOCKET NUMBER:  960296.94916
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE:  608/251-5000
9  TELEFAX:  608-251-9166
10 INFORMATION FOR SEQ ID NO:  12:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH:  3418 base pairs
13 TYPE:  nucleic acid
14 STRANDEDNESS:  double
15 TOPOLOGY:  circular
16 MOLECULE TYPE:  other nucleic acid
17 DESCRIPTION:  /desc = "Plasmid prZ7075
18 US-08-944-916-12

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Query Match	92.4%	Score 462;	DB 2;	Length 3418;
Best Local Similarity	99.2%;	Pred. No. 1.6e-150;		
Matches 496;	Conservative 0;	Mismatches 0;	Indels 4;	Gaps 3;
QY	1	ATATATGAGTAACCTTGGTCTGACAGTTCACCAATGCTTAATCAGTAGGACACCTATCTCA	60	
DB	2326	ATATATGAGTAACCTTGGTCTGACAGTTCACCAATGCTTAATCAGTAGGACACCTATCTCA	2385	
QY	61	GCAGATCTGTCTATTTCGTTTCATCCCATAGTTGCTGCAACTTCCCCGTCGTTAGATAACT	120	
DB	2386	GCAGATCTGTCTATTTCGTTTCAT--CCATAGTTGCTG--ACTCCCGTCGTTAGATAACT	2442	
QY	121	ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAAGACCCACG	180	
DB	2443	ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCG--AGACCCACG	2501	
QY	181	CTCACGGCTCCAGATTATCAGCAATAAACCCAGCCAGCCGGAAGGCCCGAGCGCAGAAG	240	
DB	2502	CTCACGGCTCCAGATTATCAGCAATAAACCCAGCCAGCCGGAAGGCCCGAGCGCAGAAG	2561	
QY	241	TGTCCTGTGCAACTTTATCCGCCCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT	300	
DB	2562	TGTCCTGTGCAACTTTATCCGCCCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT	2621	
QY	301	AAGTAGTTGCCAGTTAATAGTTTGGCGAACGTTGTGCCATTGCTGCAGGCATCTGTGT	360	
DB	2622	AAGTAGTTGCCAGTTAATAGTTTGGCGAACGTTGTGCCATTGCTGCAGGCATCTGTGT	2681	
QY	361	GTCAACGCTCGTCGTTGGTATGCTTCATTCAGCTCGGTTCCCAACGATCAAGGCGAGT	420	
DB	2682	GTCAACGCTCGTCGTTGGTATGCTTCATTCAGCTCGGTTCCCAACGATCAAGGCGAGT	2741	
QY	421	TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGTCTCCTTCGGTCTCTCCGATCTGTTG	480	
DB	2742	TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGTCTCCTTCGGTCTCTCCGATCTGTTG	2801	
QY	481	CAGAAGTAAGTTGGCCGCGAG	500	
DB	2802	CAGAAGTAAGTTGGCCGCGAG	2821	

RESULT 9
US-09-058-483-9
: Sequence 9, Application US/09058483A
: Patent No. 6365347
: GENERAL INFORMATION:
: APPLICANT: Murray, Andrew W.
: APPLICANT: Smith, Dana L.
: APPLICANT: Sorger, Peter K.
: APPLICANT: No. 6365347man, Thea C.
: TITLE OF INVENTION: METHODS FOR IDENTIFYING
: TITLE OF INVENTION: PATHWAYS USING COMPARATIVE
: FILE REFERENCE: 30432.1US11
: CURRENT APPLICATION NUMBER: US/09/058-483-9

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; CURRENT FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 08/835,727
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 3516
; TYPE: DNA
; ORGANISM: nucleic acid sequence of pSF248 plasmid
US-09-058-493-9

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Query Match	92.4%	Score 462;	DB 3;	Length 3516;
Best Local Similarity	99.2%;	Pred. No. 1.6e-150;		
Matches 496;	Conservative 0;	Mismatches 0;	Indels 4;	Gaps 3;
Qy	1	ATATATGAGTAAACTTTGGTCTGACAGTTACCAATGCTTAATCAGTGGGACCTATCTCA	60	
Db	2425	ATATATGAGTAAACTTTGGTCTGACAGTTACCAATGCTTAATCAGTGGGACCTATCTCA	2484	
Qy	61	GGCATCTGTCTATTTTCGTTTCATCCCATAGTTGCTGCAACTCCCGGTCGTTAGATAACT	120	
Db	2485	GGCATCTGTCTATTTTCGTTTCAT--CCATAGTTGCTG--ACTCCCGTCGTTAGATAACT	2541	
Qy	121	ACGATACGGAGGGCTTACCATCTGCGCCCGAGTGTGCAATGATACCGCGAAGACCCACG	180	
Db	2542	ACGATACGGAGGGCTTACCATCTGCGCCCGAGTGTGCAATGATACCGCG-AGACCCACG	2600	
Qy	181	CTCACCGGCTCCAGATTTATCAGCAATAAACACGACGCGGGAAGGGCCGAGCGCAGAAG	240	
Db	2601	CTCACCGGCTCCAGATTTATCAGCAATAAACACGACGCGGGAAGGGCCGAGCGCAGAAG	2660	
Qy	241	TGTCCTCTGCAACTTTTATCCGCTCCATCCAGTCTATTAAATTGTTGCGGGAAGCTAGAGT	300	
Db	2661	TGTCCTCTGCAACTTTTATCCGCTCCATCCAGTCTATTAAATTGTTGCGGGAAGCTAGAGT	2720	
Qy	301	AAGTAGTTCGCAGTTAAATAGTTTGGCAACCGTTGTGCCATTTGTCAGGCCATCGTGGT	360	
Db	2721	AAGTAGTTCGCAGTTAAATAGTTTGGCAACCGTTGTGCCATTTGTCAGGCCATCGTGGT	2780	
Qy	361	GTACGCTCGTGTGGTATAGCTTCATTTCAGCTCCGGTCCCAACGATCAAGGCGAGT	420	
Db	2781	GTACGCTCGTGTGGTATAGCTTCATTTCAGCTCCGGTCCCAACGATCAAGGCGAGT	2840	
Qy	421	TACATGATCCCCCATGTTGTGCAGAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGT	480	
Db	2841	TACATGATCCCCCATGTTGTGCAGAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGT	2900	
Qy	481	CAGAGTAAGTTGGCGCGAG	500	
Db	2901	CAGAGTAAGTTGGCGCGAG	2920	

```

RESULT 10
US-08-232-463-8/c
; Sequence 8, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHNEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: US/07/935,313
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3656 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pFS50
US-08-232-463-8

Query Match 92.4%; Score 462; DB 1; Length 3656;
Best Local Similarity 99.2%; Pred. No. 1.7e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTAGGACCTATCTCA 60
DB 2742 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTAGGACCTATCTCA 2683
QY 61 GCGATCTGTCTATTTTCGTTTCATCCCAATGCTGCTGCAACTCCCGTCTGTAGATAACT 120
DB 2682 GCGATCTGTCTATTTTCGTTTCAT-CCATAGTTGCTG-ACTCCCGTCTGTAGATAACT 2626
QY 121 ACGATACGGGAGGGCTTACCATCTGCGCCCGAGTCTGCAATGATACCGGAGACCCAG 180
DB 2625 ACGATACGGGAGGGCTTACCATCTGCGCCCGAGTCTGCAATGATACCGGAGACCCAG 2567
QY 181 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCCGAGGCGGAGCGCAGAAG 240
DB 2566 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCCGAGGCGGAGCGCAGAAG 2507
QY 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 300
DB 2506 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 2447
QY 301 AAGTAGTTCGCCAGTAAATAGTTTGGCAACGTTTGGCAATGCTGCTGCGGCAATCGTGT 360
DB 2446 AAGTAGTTCGCCAGTAAATAGTTTGGCAACGTTTGGCAATGCTGCTGCGGCAATCGTGT 2387
QY 361 GTCACGCTCGTCTGTGGTATGCTTCATTCAGTCTCGGTTTCCCAACGATCAAGGCGAGT 420
DB 2386 GTCACGCTCGTCTGTGGTATGCTTCATTCAGTCTCGGTTTCCCAACGATCAAGGCGAGT 2327
QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTAGCTCTTCGCTCCGATCGTGTGT 480
DB 2326 TACATGATCCCCCATGTTGTGCAAAAAGCGGTAGCTCTTCGCTCCGATCGTGTGT 2267
QY 481 CAGAGTAAAGTTGGCCGAG 500
DB 2266 CAGAGTAAAGTTGGCCGAG 2247

RESULT 11
US-08-232-463-9/c
; Sequence 9, Application US/08232463
; Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3688 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pFS51
US-08-232-463-9

Query Match 92.4%; Score 462; DB 1; Length 3688;
Best Local Similarity 99.2%; Pred. No. 1.7e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTAGGACCTATCTCA 60
DB 2774 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTAGGACCTATCTCA 2715
QY 61 GCGATCTGTCTATTTTCGTTTCATCCCAATGCTGCTGCAACTCCCGTCTGTAGATAACT 120
DB 2714 GCGATCTGTCTATTTTCGTTTCAT-CCATAGTTGCTG-ACTCCCGTCTGTAGATAACT 2658
QY 121 ACGATACGGGAGGGCTTACCATCTGCGCCCGAGTCTGCAATGATACCGGAGACCCAG 180
DB 2657 ACGATACGGGAGGGCTTACCATCTGCGCCCGAGTCTGCAATGATACCGGAGACCCAG 2599
QY 181 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCCGAGGCGGAGCGCAGAAG 240
DB 2598 CTCACCGGCTCCAGATTTATCAGCAATAAACACGAGCCGAGGCGGAGCGCAGAAG 2539
QY 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 300
DB 2538 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAAGCTAGAGT 2479
QY 301 AAGTAGTTCGCCAGTAAATAGTTTGGCAACGTTTGGCAATGCTGCTGCGGCAATCGTGT 360
DB 2478 AAGTAGTTCGCCAGTAAATAGTTTGGCAACGTTTGGCAATGCTGCTGCGGCAATCGTGT 2419

361 GTCACGCTCGTGGTTGGTATGGCTTCATTACAGTCCGGTTCCCAAGCATCAAGCGAGT 420
2418 GTCACGCTCGTGGTTGGTATGGCTTCATTACAGTCCGGTTCCCAAGCATCAAGCGAGT 2359
421 TACATGATCCCGCATGTTGTCACAAAAGCGGTAGTCTTCCGTCCTCGATCGTTGT 480
2358 TACATGATCCCGCATGTTGTCACAAAAGCGGTAGTCTTCCGTCCTCGATCGTTGT 2299
481 CAGAAGTAAGTTGGCCGCGAG 500
2298 CAGAAGTAAGTTGGCCGCGAG 2279
RESULT 12
US-07-834-539A-49
; Sequence 49, Application US/07834539A
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/834,539A
; FILING DATE: 1992-02-05
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3698 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-834-539A-49
Query Match 92.4%; Score 462; DB 1; Length 3698;
Best Local Similarity 99.2%; Pred. No. 1.7e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
DB 2606 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 2665
QY 61 GCGATCTGCTATTTTCGTTTCATCCCATCCATGTTGCTGCAACTCCCGCTGTGTAGATAACT 120
DB 2666 GCGATCTGCTATTTTCGTTTCAT-CCATAGTTGCTG--ACTCCCGCTGTGTAGATAACT 2722
QY 121 ACGATACGGAGGGCTTACCATCTGCCCCAGTCTGCAATGATATACCGGAGAGCCCGAG 180
DB 2723 ACGATACGGAGGGCTTACCATCTGCCCCAGTCTGCAATGATATACCGG-AGACCCAG 2781
QY 181 CTCACCGGCTCCAGATTTTATCAGCAATAAACCAGCGAGCGGAAAGGCGGAGCGAGAG 240
DB 2782 CTCACCGGCTCCAGATTTTATCAGCAATAAACCAGCGAGCGGAAAGGCGGAGCGAGAG 2841

241 TGGTCTCGCAACTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAGCTAGAGT 300
2842 TGGTCTCGCAACTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAGCTAGAGT 2901
301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTCAGGCATCGTGT 360
2902 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTCAGGCATCGTGT 2961
361 GTCACGCTCGTGGTTGGTATGGCTTCATTACGTCGGTTCCCAAGCATCAAGCGAGT 420
2962 GTCACGCTCGTGGTTGGTATGGCTTCATTACGTCGGTTCCCAAGCATCAAGCGAGT 3021
421 TACATGATCCCGCATGTTGTCACAAAAGCGGTAGTCTTCCGTCCTCGATCGTTGT 480
3022 TACATGATCCCGCATGTTGTCACAAAAGCGGTAGTCTTCCGTCCTCGATCGTTGT 3081
481 CAGAAGTAAGTTGGCCGCGAG 500
3082 CAGAAGTAAGTTGGCCGCGAG 3101
RESULT 13
US-08-800-353-49
; Sequence 49, Application US/08800353
; Patent No. 5874299
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5874299-Human Animals Capable of
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,353
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/834,539
; FILING DATE: 1992-02-05
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3698 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-800-353-49
Query Match 92.4%; Score 462; DB 2; Length 3698;
Best Local Similarity 99.2%; Pred. No. 1.7e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60

Db 2606 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCA 2665
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Db 2666 GCGATCTGTCTATTTCGTTTCAT-CCATAGTTGCTG--ACTCCCGTGGTAGATAACT 2722
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Db 2723 ACGNATCGGAGGGCTTACCACTTGGGCCCGACAGTCTGCTCAATGATACCGG-AGACCCACG 2781
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Qy 301 AAGTAGTTCGCGAGTTAATAGTTTGGCGAAGGTTGTTGCCATTGCTCGAGGCACTGGT 360
Db 2902 AAGTAGTTCGCGAGTTAATAGTTTGGCGAAGGTTGTTGCCATTGCTCGAGGCACTGGT 2961
Qy 361 GTCACGCTCGTGGTTCGTTGCTTCCATTCAGCTCCGCTTCCCAAGGCGAGT 420
Db 2962 GTCACGCTCGTGGTTCGTTGCTTCCATTCAGCTCCGCTTCCCAAGGCGAGT 3021
Qy 421 TACATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCGGCTCCCGATCGTTGT 480
Db 3022 TACATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCGGCTCCCGATCGTTGT 3081
Qy 481 CAGAAGTAAGTTGGCGCGAG 500
Db 3082 CAGAAGTAAGTTGGCGCGAG 3101

RESULT 14

PCT-US92-06185-49
; Sequence 49, Application PC/TUS9206185
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06185
; FILING DATE: 19910828
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 87654
; REFERENCE/DOCKET NUMBER: 14643-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3698 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
PCT-US92-06185-49
Query Match 92.4%; Score 462; DB 5; Length 3698;
Best Local Similarity 99.2%; Pred. No. 1.7e-150; Mismatches 0; Indels 4; Gaps 3;
Matches 496; Conservative 0;
Qy 1 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCA 60
Db 2606 ATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCA 2665
Qy 61 GCGATCTGTCTATTTCGTTTCATCCATCCAGTCTGCTCAACTCCCGCGTGGTAGATAACT 120
Db 2666 GCGATCTGTCTATTTCGTTTCAT-CCATAGTTGCTG--ACTCCCGTGGTAGATAACT 2722
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Db 2962 GTCACGCTCGTGGTTCGTTGCTTCCATTCAGCTCCGCTTCCCAAGGCGAGT 3021
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Db 3022 TACATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCTCGGCTCCCGATCGTTGT 3081
Qy 481 CAGAAGTAAGTTGGCGCGAG 500
Db 3082 CAGAAGTAAGTTGGCGCGAG 3101
RESULT 15
US-08-053-131-120
; Sequence 120, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 3699 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-053-131-120

Query Match 92.4%; Score 462; DB 1; Length 3699;
Best Local Similarity 99.2%; Pred. No. 1.7e-150;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
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QY 61 GCGATCTGCTATTTCGTTTCATCCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT 120
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QY 2667 GCGATCTGCTATTTCGTTTCAT - CCAATGTTGCTG - ACTCCCGCTCGTGTAGATAACT 2723
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QY 121 ACCGATCGGAGGGCTTACCATTGCGCCCGAGTCTGCAATGATACGGGAAGACCCACG 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2724 ACCGATCGGAGGGCTTACCATTGCGCCCGAGTCTGCAATGATACCGCG - AGACCCACG 2782
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2783 CTCACGGCTCCAGATTATCAGCAATAAACACGACGCGAAGCGGCGAGCGAGAAG 2842
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QY 2903 AAGTAGTTGCCAGTTAAATAGTTTGGCAACGTTGTTGCCATTGCTGCAGGCATCGTGT 2962
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QY 421 TACATGATCCCCCATGTTGTGCAAAAAGGGTTAGTCTCTTCGGTCTCCGATCGTTGT 480
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QY 481 CAGAAGTAAGTTGGCGGCAG 500
DB ||||||||||||||||||||
QY 3083 CAGAAGTAAGTTGGCGGCAG 3102
DB ||||||||||||||||||||

Search completed: April 29, 2005, 05:17:46
Job time : 155 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 03:41:23 ; Search time 2574 Seconds
(without alignments)

1182.534 Million cell updates/sec

Title: US-10-043-160-5_COPY_1_500

Perfect score: 500

Sequence: 1 atatagagtaaaacttggtc.....cagaagtaagtggccgcag 500

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	100.0	43228	18	US-10-043-160-5
2	462	92.4	1086	16	US-10-182-616-11
3	462	92.4	2212	10	US-09-764-891-5577
4	462	92.4	2212	10	US-09-764-891-5577
5	462	92.4	2213	9	US-09-764-868-1456
6	462	92.4	2213	9	US-09-764-868-1456
7	462	92.4	2213	10	US-09-764-891-5570
8	462	92.4	2213	10	US-09-764-891-5572
9	462	92.4	2213	10	US-09-764-891-5560
10	462	92.4	2213	10	US-09-764-891-5560
11	462	92.4	3159	9	US-09-948-939-1

12	462	92.4	3159	15	US-10-324-493-4	Sequence 4, Appli
13	462	92.4	4021	10	US-09-883-573-1	Sequence 1, Appli
14	462	92.4	4100	9	US-09-813-718-5	Sequence 5, Appli
15	462	92.4	4100	17	US-10-240-532-5	Sequence 5, Appli
16	462	92.4	4100	18	US-10-240-527A-5	Sequence 5, Appli
17	462	92.4	4231	8	US-08-901-062-2	Sequence 2, Appli
18	462	92.4	4257	15	US-10-161-403-30	Sequence 30, Appli
19	462	92.4	4257	18	US-10-161-408-22	Sequence 22, Appli
20	462	92.4	4458	16	US-10-270-487-52	Sequence 52, Appli
21	462	92.4	4458	18	US-10-742-634-14	Sequence 14, Appli
22	462	92.4	4557	17	US-10-457-372-5	GENERAL INFORMA
23	462	92.4	4682	9	US-09-813-718-3	Sequence 3, Appli
24	462	92.4	4682	9	US-09-813-718-7	Sequence 7, Appli
25	462	92.4	4682	17	US-10-240-532-3	Sequence 7, Appli
26	462	92.4	4682	17	US-10-240-532-7	Sequence 3, Appli
27	462	92.4	4682	18	US-10-240-527A-3	Sequence 7, Appli
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30	462	92.4	4742	14	US-10-080-833-6	Sequence 15, Appli
31	462	92.4	4742	17	US-10-240-532-15	Sequence 15, Appli
32	462	92.4	4742	18	US-10-240-527A-15	Sequence 1, Appli
33	462	92.4	4742	18	US-10-628-783-1	Sequence 1, Appli
34	462	92.4	4742	19	US-10-833-743-1	Sequence 4, Appli
35	462	92.4	4752	17	US-10-383-846-4	Sequence 13, Appli
36	462	92.4	4811	9	US-09-813-718-13	Sequence 4, Appli
37	462	92.4	4811	14	US-10-080-833-4	Sequence 13, Appli
38	462	92.4	4811	17	US-10-240-532-13	Sequence 13, Appli
39	462	92.4	4811	18	US-10-240-527A-13	Sequence 11, Appli
40	462	92.4	4877	9	US-09-813-718-11	Sequence 2, Appli
41	462	92.4	4877	14	US-10-080-833-2	Sequence 11, Appli
42	462	92.4	4877	17	US-10-240-532-11	Sequence 11, Appli
43	462	92.4	4877	18	US-10-240-527A-11	Sequence 20, Appli
44	462	92.4	4884	18	US-10-622-220-20	Sequence 19, Appli
45	462	92.4	4899	18	US-10-600-790-19	

ALIGNMENTS

RESULT 1

US-10-043-160-5
; Sequence 5, Application US/10043160
; Publication No. US20040170952A1
; GENERAL INFORMATION:
; APPLICANT: ZOOBIO, RIMA
; APPLICANT: AUFRAY, CHARLES
; APPLICANT: CHAUSSE, ANNE-MARIE
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTING GENES RELATED TO
; TITLE OF INVENTION: MAJOR HISTOCOMPATIBILITY COMPLEX OF DOMESTIC FOWL, SUCH
; FILE REFERENCE: 1721-22
; CURRENT APPLICATION NUMBER: US/10/043,160
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 09/554,911
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: PCT/FR98/02501
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: FR 97/14669
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 43228
; TYPE: DNA
; ORGANISM: Gallus sp.
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(43228)
; OTHER INFORMATION: "n" represents a, t, c, g, other or unknown
US-10-043-160-5

Query Match 100.0%; Score 500; DB 18; Length 43228;
Best Local Similarity 100.0%; Pred. No. 6.1e-162;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 ATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCATGTCAGTGAGGACCTATCTCA 60
 QY 61 GCGATCTGCTATTTTGGTTCATCCCATAGTTCCTGCAACTCCCGTCGCTGCTAGATAAAT 120
 Db 61 GCGATCTGCTATTTTGGTTCATCCCATAGTTCCTGCAACTCCCGTCGCTGCTAGATAAAT 120
 QY 121 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAAGCCACG 180
 Db 121 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAAGCCACG 180
 QY 181 CTCACGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGCCGAGCGAGAAG 240
 Db 181 CTCACGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGCCGAGCGAGAAG 240
 QY 241 TGGTCTGCAACTTTATCGCCCTCCATCCAGTCTTATTAATTTGTCGGGAAGCTAGAGT 300
 Db 241 TGGTCTGCAACTTTATCGCCCTCCATCCAGTCTTATTAATTTGTCGGGAAGCTAGAGT 300
 QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTCGAGGCATCGTGT 360
 Db 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTCGAGGCATCGTGT 360
 QY 361 GTCACGCTCGTGTGGTATGCTTCATTCAGCTCGGTTCCCAAGATCAAGGCGAGT 420
 Db 361 GTCACGCTCGTGTGGTATGCTTCATTCAGCTCGGTTCCCAAGATCAAGGCGAGT 420
 QY 421 TACATGATCCCCCATGTTGTCGCAAAAGGGTTAGTCTCTCGGTCCTCCGATCGTGT 480
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 QY 481 CAGAAGTAAGTTGGCGCGAG 500
 Db 481 CAGAAGTAAGTTGGCGCGAG 500

RESULT 2
 US-10-182-616-11
 ; Sequence 11, Application US/10182616
 ; Publication No. US20030159184A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sakata Seed Corporation et al.
 ; TITLE OF INVENTION: Methods and Constructs for Plant Transformation
 ; FILE REFERENCE: 78592-3
 ; CURRENT APPLICATION NUMBER: US/10/182,616
 ; CURRENT FILING DATE: 2002-08-01
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 11
 ; TYPE: DNA
 ; LENGTH: 1086
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Ampicillin resistance gene: pBR322 GenBank Accession No. US20030159184A1
 ; OTHER INFORMATION: 3265-4350
 US-10-182-616-11

Query Match 92.4%; Score 462; DB 16; Length 1086;
 Best Local Similarity 99.2%; Pred. No. 1.9e-149;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

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 QY 61 GCGATCTGCTATTTTGGTTCATCCCATAGTTCCTGCAACTCCCGTCGCTGCTAGATAAAT 120
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 Db 239 TGGTCTGCAACTTTATCGCCCTCCATCCAGTCTTATTAATTTGTCGGGAAGCTAGAGT 298
 QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTCGAGGCATCGTGT 360
 Db 299 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTCGAGGCATCGTGT 358
 QY 361 GTCACGCTCGTGTGGTATGCTTCATTCAGCTCGGTTCCCAAGATCAAGGCGAGT 420
 Db 359 GTCACGCTCGTGTGGTATGCTTCATTCAGCTCGGTTCCCAAGATCAAGGCGAGT 418
 QY 421 TACATGATCCCCCATGTTGTCGCAAAAGGGTTAGTCTCTCGGTCCTCCGATCGTGT 480
 Db 419 TACATGATCCCCCATGTTGTCGCAAAAGGGTTAGTCTCTCGGTCCTCCGATCGTGT 478
 QY 481 CAGAAGTAAGTTGGCGCGAG 500
 Db 479 CAGAAGTAAGTTGGCGCGAG 498

RESULT 3
 US-09-764-891-5577/c
 ; Sequence 5577, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5577
 ; LENGTH: 2212
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-891-5577

Query Match 92.4%; Score 462; DB 10; Length 2212;
 Best Local Similarity 99.2%; Pred. No. 2.6e-149;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

QY 1 ATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCATGTCAGTGAGGACCTATCTCA 60
 Db 1098 ATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCATGTCAGTGAGGACCTATCTCA 1039
 QY 61 GCGATCTGCTATTTTGGTTCATCCCATAGTTCCTCGCAACTCCCGTCGCTAGATAAAT 120
 Db 1038 GCGATCTGCTATTTTGGTTCATCCCATAGTTCCTCGCAACTCCCGTCGCTAGATAAAT 982
 QY 121 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAAGCCACG 180
 Db 981 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCG-AGACCCACG 923
 QY 181 CTCACGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGCCGAGCGAGAAG 240
 Db 922 CTCACGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGCCGAGCGAGAAG 863
 QY 241 TGGTCTGCAACTTTATCGCCCTCCATCCAGTCTTATTAATTTGTCGGGAAGCTAGAGT 300
 Db 862 TGGTCTGCAACTTTATCGCCCTCCATCCAGTCTTATTAATTTGTCGGGAAGCTAGAGT 803
 QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTCGAGGCATCGTGT 360

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Db      802 AAGTAGTTCGCCAGTTAATAGTTGGCCAAAGTTGTTGCCATTGCTGCCAGGCATCGTGT 743
Qy      361 GTCACGCTCGTCTGTTGGTATAGCTTCATTAGCTCCGGTTCCCAACGATCAAGGCGAGT 420
Db      742 GTCACGCTCGTCTGTTGGTATAGCTTCATTAGCTCCGGTTCCCAACGATCAAGGCGAGT 683
Qy      421 TACATGATCCCCCATGTTGTCGCAAAAAGCGGTAGCTCCTTCGGTCTCCGATCGTTGT 480
Db      682 TACATGATCCCCCATGTTGTCGCAAAAAGCGGTAGCTCCTTCGGTCTCCGATCGTTGT 623
Qy      481 CAGAAGTAAGTTGGCCGCGAG 500
Db      622 CAGAAGTAAGTTGGCCGCGAG 603

RESULT 4
US-09-764-891-5607/c
; Sequence 5607, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5607
; LENGTH: 2212
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-5607

Query Match          92.4%; Score 462; DB 10; Length 2212;
Best Local Similarity 99.2%; Pred. No. 2.6e-149;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

Qy      1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGAGGACCTATCTCA 60
Db      1098 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGAGGACCTATCTCA 1039
Qy      61 GCGATCTGCTATTTGCTTCATCCCATAGTTCCCTGCAACTCCCGTCTGTTAGATAACT 120
Db      1038 GCGATCTGCTATTTGCTTCATCCCATAGTTCCCTGCAACTCCCGTCTGTTAGATAACT 982
Qy      121 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAAGACCCACG 180
Db      981 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGG-AGACCCACG 923
Qy      181 CTCACGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCGGCGCAGAAG 240
Db      922 CTCACGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCGGCGCAGAAG 863
Qy      241 TGGTCTGCAACTTTATCCGCTCCATCCAGTCTAATTAATTTGTCGGGAGCTAGAGT 300
Db      862 TGGTCTGCAACTTTATCCGCTCCATCCAGTCTAATTAATTTGTCGGGAGCTAGAGT 803
Qy      301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCATTTGTCAGGATCGTGT 360
Db      802 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCATTTGTCAGGATCGTGT 743
Qy      361 GTCACGCTCGTCTGTTGGTATGCTTTCATTGAGTCCGTTCCCAACGATCAAGGCGAGT 420
Db      742 GTCACGCTCGTCTGTTGGTATGCTTTCATTGAGTCCGTTCCCAACGATCAAGGCGAGT 683
Qy      421 TACATGATCCCCCATGTTGTCGCAAAAAGCGGTAGCTCCTTCGGTCTCCGATCGTTGT 480
Db      682 TACATGATCCCCCATGTTGTCGCAAAAAGCGGTAGCTCCTTCGGTCTCCGATCGTTGT 623
Qy      481 CAGAAGTAAGTTGGCCGCGAG 500
Db      622 CAGAAGTAAGTTGGCCGCGAG 603

Query Match          92.4%; Score 462; DB 10; Length 2212;
Best Local Similarity 99.2%; Pred. No. 2.6e-149;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

Qy      1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGAGGACCTATCTCA 60
Db      1098 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGAGGACCTATCTCA 1039
Qy      61 GCGATCTGCTATTTGCTTCATCCCATAGTTCCCTGCAACTCCCGTCTGTTAGATAACT 120
Db      1038 GCGATCTGCTATTTGCTTCATCCCATAGTTCCCTGCAACTCCCGTCTGTTAGATAACT 982
Qy      121 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAAGACCCACG 180
Db      981 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGG-AGACCCACG 923
Qy      181 CTCACGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCGGCGCAGAAG 240
Db      922 CTCACGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCGGCGCAGAAG 863
Qy      241 TGGTCTGCAACTTTATCCGCTCCATCCAGTCTAATTAATTTGTCGGGAGCTAGAGT 300
Db      862 TGGTCTGCAACTTTATCCGCTCCATCCAGTCTAATTAATTTGTCGGGAGCTAGAGT 803
Qy      301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCATTTGTCAGGATCGTGT 360
Db      802 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCATTTGTCAGGATCGTGT 743
Qy      361 GTCACGCTCGTCTGTTGGTATGCTTTCATTGAGTCCGTTCCCAACGATCAAGGCGAGT 420
Db      742 GTCACGCTCGTCTGTTGGTATGCTTTCATTGAGTCCGTTCCCAACGATCAAGGCGAGT 683
Qy      421 TACATGATCCCCCATGTTGTCGCAAAAAGCGGTAGCTCCTTCGGTCTCCGATCGTTGT 480
Db      682 TACATGATCCCCCATGTTGTCGCAAAAAGCGGTAGCTCCTTCGGTCTCCGATCGTTGT 623
Qy      481 CAGAAGTAAGTTGGCCGCGAG 500
Db      622 CAGAAGTAAGTTGGCCGCGAG 603

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RESULT 5
US-09-764-868-1456/c
; Sequence 1456, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1456
; LENGTH: 2213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1456

Query Match          92.4%; Score 462; DB 9; Length 2213;
Best Local Similarity 99.2%; Pred. No. 2.6e-149;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

Qy      1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGAGGACCTATCTCA 60
Db      1098 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGAGGACCTATCTCA 1039
Qy      61 GCGATCTGCTATTTGCTTCATCCCATAGTTCCCTGCAACTCCCGTCTGTTAGATAACT 120
Db      1038 GCGATCTGCTATTTGCTTCATCCCATAGTTCCCTGCAACTCCCGTCTGTTAGATAACT 982
Qy      121 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAAGACCCACG 180
Db      981 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGG-AGACCCACG 923
Qy      181 CTCACGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCGGCGCAGAAG 240
Db      922 CTCACGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCGGCGCAGAAG 863
Qy      241 TGGTCTGCAACTTTATCCGCTCCATCCAGTCTAATTAATTTGTCGGGAGCTAGAGT 300
Db      862 TGGTCTGCAACTTTATCCGCTCCATCCAGTCTAATTAATTTGTCGGGAGCTAGAGT 803
Qy      301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCATTTGTCAGGATCGTGT 360
Db      802 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTCATTTGTCAGGATCGTGT 743
Qy      361 GTCACGCTCGTCTGTTGGTATGCTTTCATTGAGTCCGTTCCCAACGATCAAGGCGAGT 420
Db      742 GTCACGCTCGTCTGTTGGTATGCTTTCATTGAGTCCGTTCCCAACGATCAAGGCGAGT 683
Qy      421 TACATGATCCCCCATGTTGTCGCAAAAAGCGGTAGCTCCTTCGGTCTCCGATCGTTGT 480
Db      682 TACATGATCCCCCATGTTGTCGCAAAAAGCGGTAGCTCCTTCGGTCTCCGATCGTTGT 623
Qy      481 CAGAAGTAAGTTGGCCGCGAG 500
Db      622 CAGAAGTAAGTTGGCCGCGAG 603

RESULT 6
US-09-764-868-1462/c
; Sequence 1462, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper

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NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1462
; LENGTH: 2213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1462

Query Match 92.4%; Score 462; DB 9; Length 2213;
Best Local Similarity 99.2%; Pred. No. 2.6e-149;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
DB 1098 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 1039
QY 61 GCGATCTGTCTATTTTGGTTTATCCCATAGTTGCTGCAACTCCCGTCTGTGTAGATAACT 120
DB 1038 GCGATCTGTCTATTTTGGTTTATCCCATAGTTGCTGCAACTCCCGTCTGTGTAGATAACT 982
QY 121 ACGATACGGAGGGCTTACCATCTGGCCCAAGTCTGCAATGATACCGGAGACCCACG 180
DB 981 ACGATACGGAGGGCTTACCATCTGGCCCAAGTCTGCAATGATACCGGAGACCCACG 923
QY 181 CTCACCGGCTCCAGATTATCAGCAATAAACACGAGCGGAGCGCGCAGAG 240
DB 922 CTCACCGGCTCCAGATTATCAGCAATAAACACGAGCGGAGCGCGCAGAG 863
QY 241 TGGTCTCTGCAACTTTATCGGCTTCCATCCAGTCTTAATTAATTTGTCGGGAACTAGAGT 300
DB 862 TGGTCTCTGCAACTTTATCGGCTTCCATCCAGTCTTAATTAATTTGTCGGGAACTAGAGT 803
QY 301 AAGTAGTTCGCGAGTTTATCGGCTTCCATCCAGTCTTAATTAATTTGTCGGGAACTAGAGT 360
DB 802 AAGTAGTTCGCGAGTTTATCGGCTTCCATCCAGTCTTAATTAATTTGTCGGGAACTAGAGT 743
QY 361 GTACGCTCTGCTTGGTATGCTTCAATTCAGTCCGCTTCCCAACGATCAAGGCGAGT 420
DB 742 GTACGCTCTGCTTGGTATGCTTCAATTCAGTCCGCTTCCCAACGATCAAGGCGAGT 683
QY 421 TACATGATCCCCCATGTTGTGCAAAAACGCGTTAGCTCTTCCGTCCTCCGATCGTTGT 480
DB 682 TACATGATCCCCCATGTTGTGCAAAAACGCGTTAGCTCTTCCGTCCTCCGATCGTTGT 623
QY 481 CAGAAGTAAAGTTGGCGCGAG 500
DB 622 CAGAAGTAAAGTTGGCGCGAG 603

RESULT 7

US-09-764-891-5570/c
; Sequence 5570, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5570
; LENGTH: 2213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-5570

Query Match 92.4%; Score 462; DB 10; Length 2213;
Best Local Similarity 99.2%; Pred. No. 2.6e-149;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60

DB 1098 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 1039
QY 61 GCGATCTGTCTATTTTGGTTTATCCCATAGTTGCTGCAACTCCCGTCTGTGTAGATAACT 120
DB 1038 GCGATCTGTCTATTTTGGTTTATCCCATAGTTGCTGCAACTCCCGTCTGTGTAGATAACT 982
QY 121 ACGATACGGAGGGCTTACCATCTGGCCCAAGTCTGCAATGATACCGGAGACCCACG 180
DB 981 ACGATACGGAGGGCTTACCATCTGGCCCAAGTCTGCAATGATACCGGAGACCCACG 923
QY 181 CTCACCGGCTCCAGATTATCAGCAATAAACACGAGCGGAGCGCGCAGAG 240
DB 922 CTCACCGGCTCCAGATTATCAGCAATAAACACGAGCGGAGCGCGCAGAG 863
QY 241 TGGTCTCTGCAACTTTATCGGCTTCCATCCAGTCTTAATTAATTTGTCGGGAACTAGAGT 300
DB 862 TGGTCTCTGCAACTTTATCGGCTTCCATCCAGTCTTAATTAATTTGTCGGGAACTAGAGT 803
QY 301 AAGTAGTTCGCGAGTTTATCGGCTTCCATCCAGTCTTAATTAATTTGTCGGGAACTAGAGT 360
DB 802 AAGTAGTTCGCGAGTTTATCGGCTTCCATCCAGTCTTAATTAATTTGTCGGGAACTAGAGT 743
QY 361 GTACGCTCTGCTTGGTATGCTTCAATTCAGTCCGCTTCCCAACGATCAAGGCGAGT 420
DB 742 GTACGCTCTGCTTGGTATGCTTCAATTCAGTCCGCTTCCCAACGATCAAGGCGAGT 683
QY 421 TACATGATCCCCCATGTTGTGCAAAAACGCGTTAGCTCTTCCGTCCTCCGATCGTTGT 480
DB 682 TACATGATCCCCCATGTTGTGCAAAAACGCGTTAGCTCTTCCGTCCTCCGATCGTTGT 623
QY 481 CAGAAGTAAAGTTGGCGCGAG 500
DB 622 CAGAAGTAAAGTTGGCGCGAG 603

RESULT 8

US-09-764-891-5572/c
; Sequence 5572, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5572
; LENGTH: 2213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-5572

Query Match 92.4%; Score 462; DB 10; Length 2213;
Best Local Similarity 99.2%; Pred. No. 2.6e-149;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
DB 1098 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 1039
QY 61 GCGATCTGTCTATTTTGGTTTATCCCATAGTTGCTGCAACTCCCGTCTGTGTAGATAACT 120
DB 1038 GCGATCTGTCTATTTTGGTTTATCCCATAGTTGCTGCAACTCCCGTCTGTGTAGATAACT 982
QY 121 ACGATACGGAGGGCTTACCATCTGGCCCAAGTCTGCAATGATACCGGAGACCCACG 180
DB 981 ACGATACGGAGGGCTTACCATCTGGCCCAAGTCTGCAATGATACCGGAGACCCACG 923
QY 181 CTCACCGGCTCCAGATTATCAGCAATAAACACGAGCGGAGCGCGCAGAG 240

Db 922 CTCACGGCTCCAGATTATACAGAAATAAACACAGCCAGCCGGAAGCCGAGCGCAGAG 863
Qy 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT 300
Db 862 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT 803
Qy 301 AAGTAGTTCGCCAGTTAAATAGTTTGGCAACAGTTGTTGCCATTGCTGCGGCAATCGTGGT 360
Db 802 AAGTAGTTCGCCAGTTAAATAGTTTGGCAACAGTTGTTGCCATTGCTGCGGCAATCGTGGT 743
Qy 361 GTCACGCTCGTCTGTTGGTATGCTTCATTCAGCTCCGCTCCCAACGATCAAGGCGAGT 420
Db 742 GTCACGCTCGTCTGTTGGTATGCTTCATTCAGCTCCGCTCCCAACGATCAAGGCGAGT 683
Qy 421 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCCGTCCTCCGATCGTTGT 480
Db 682 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCCGTCCTCCGATCGTTGT 623
Qy 481 CAGAAGTAAGTTGGCCGCAG 500
Db 622 CAGAAGTAAGTTGGCCGCAG 603

RESULT 9
US-09-764-891-5600/c
; Sequence 5600, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5600
; LENGTH: 2213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-5600

Query Match 92.4%; Score 462; DB 10; Length 2213;
Best Local Similarity 99.2%; Pred. No. 2.6e-149;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

Qy 1 ATATATGAGTAAGTCTGCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
Db 1098 ATATATGAGTAAGTCTGCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 1039

Qy 61 GCGATCTGTCTATTTCGTTCCATCCAGTGTGCTGCAACTCCCGCTCGTGTAGATAACT 120
Db 1038 GCGATCTGTCTATTTCGTTCCAT-CCATAGTTGCTG--ACTCCCGCTCGTGTAGATAACT 982

Qy 121 ACGATACGGGAGGGCTTACCATCTGCCCCAGTGTGCAATGATACCGGGAAGACCCAG 180
Db 981 ACGATACGGGAGGGCTTACCATCTGCCCCAGTGTGCAATGATACCGG-AGACCCAG 923

Qy 181 CTCACCGGCTCCAGATTTTATCAGCAATAAACACGAGCCGCGGAAGGCGGAGCAGAG 240
Db 922 CTCACCGGCTCCAGATTTTATCAGCAATAAACACGAGCCGCGGAAGGCGGAGCAGAG 863

Qy 241 TGGTCTCGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT 300
Db 862 TGGTCTCGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT 803

Qy 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACAGTTGTCCTCCGATTCAGGCGAGT 360
Db 802 AAGTAGTTCGCCAGTTAATAGTTTGGCAACAGTTGTCCTCCGATTCAGGCGAGT 743

Qy 361 GTCACGCTCGTCTGTTGGTATGCTTCATTCAGCTCCGCTCCCAACGATCAAGGCGAGT 420
Db 742 GTCACGCTCGTCTGTTGGTATGCTTCATTCAGCTCCGCTCCCAACGATCAAGGCGAGT 683

Qy 421 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCCGTCCTCCGATCGTTGT 480
Db 682 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCCGTCCTCCGATCGTTGT 623

Qy 481 CAGAAGTAAGTTGGCCGCAG 500
Db 622 CAGAAGTAAGTTGGCCGCAG 603

RESULT 11
US-09-948-939-1
; Sequence 1, Application US/09948939

Db 922 CTCACGGCTCCAGATTATACAGAAATAAACACAGCCAGCCGGAAGCCGAGCGCAGAG 863
Qy 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT 300
Db 862 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT 803
Qy 301 AAGTAGTTCGCCAGTTAAATAGTTTGGCAACAGTTGTTGCCATTGCTGCGGCAATCGTGGT 360
Db 802 AAGTAGTTCGCCAGTTAAATAGTTTGGCAACAGTTGTTGCCATTGCTGCGGCAATCGTGGT 743
Qy 361 GTCACGCTCGTCTGTTGGTATGCTTCATTCAGCTCCGCTCCCAACGATCAAGGCGAGT 420
Db 742 GTCACGCTCGTCTGTTGGTATGCTTCATTCAGCTCCGCTCCCAACGATCAAGGCGAGT 683
Qy 421 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCCGTCCTCCGATCGTTGT 480
Db 682 TACATGATCCCCCATGTTGTGCAAAAAGCGTTAGTCTCTCCGTCCTCCGATCGTTGT 623
Qy 481 CAGAAGTAAGTTGGCCGCAG 500
Db 622 CAGAAGTAAGTTGGCCGCAG 603

RESULT 9
US-09-764-891-5600/c
; Sequence 5600, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5600
; LENGTH: 2213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-5600

Query Match 92.4%; Score 462; DB 10; Length 2213;
Best Local Similarity 99.2%; Pred. No. 2.6e-149;
Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

Qy 1 ATATATGAGTAAGTCTGCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 60
Db 1098 ATATATGAGTAAGTCTGCTGACAGTTACCAATGCTTAATCAGTGAGGACCTATCTCA 1039

Qy 61 GCGATCTGTCTATTTCGTTCCATCCAGTGTGCTGCAACTCCCGCTCGTGTAGATAACT 120
Db 1038 GCGATCTGTCTATTTCGTTCCAT-CCATAGTTGCTG--ACTCCCGCTCGTGTAGATAACT 982

Qy 121 ACGATACGGGAGGGCTTACCATCTGCCCCAGTGTGCAATGATACCGGGAAGACCCAG 180
Db 981 ACGATACGGGAGGGCTTACCATCTGCCCCAGTGTGCAATGATACCGG-AGACCCAG 923

Qy 181 CTCACCGGCTCCAGATTTTATCAGCAATAAACACGAGCCGCGGAAGGCGGAGCAGAG 240
Db 922 CTCACCGGCTCCAGATTTTATCAGCAATAAACACGAGCCGCGGAAGGCGGAGCAGAG 863

Qy 241 TGGTCTCGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT 300
Db 862 TGGTCTCGCAACTTTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGT 803

Qy 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACAGTTGTTGCCATTGCTGCGGCAATCGTGGT 360
Db 802 AAGTAGTTCGCCAGTTAATAGTTTGGCAACAGTTGTTGCCATTGCTGCGGCAATCGTGGT 743

Qy 361 GTCACGCTCGTCTGTTGGTATGCTTCATTCAGCTCCGCTCCCAACGATCAAGGCGAGT 420
Db 742 GTCACGCTCGTCTGTTGGTATGCTTCATTCAGCTCCGCTCCCAACGATCAAGGCGAGT 683

; TITLE OF INVENTION: Organic Compounds
 ; FILE REFERENCE: 4-31471
 ; CURRENT APPLICATION NUMBER: US/09/883,573
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/213,132
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 60/286,949
 ; PRIOR FILING DATE: 2001-02-07
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 4021
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: plasmid
 US-09-883-573-1

Query Match 92.4%; Score 462; DB 10; Length 4021;
 Best Local Similarity 99.2%; Pred. No. 3.4e-149;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
 QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGGAGGACCTACTCTCA 60
 DB 2829 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGGAGGACCTACTCTCA 2888
 QY 61 GCGATCTGTCTATTTCGTTTCATCCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT 120
 DB 2889 GCGATCTGTCTATTTCGTTTCAT -CCATAGTTGCTG -ACTCCCGCTCGTGTAGATAACT 2945
 QY 121 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCAAGACCCACG 180
 DB 2946 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCG -AGACCCACG 3004
 QY 181 CTCACGGCTCCAGATTATCAGCAATAAACACGAGCCGAGCGGAGCGGAGGAG 240
 DB 3005 CTCACGGCTCCAGATTATCAGCAATAAACACGAGCCGAGCGGAGGAGGAGGAGGAG 3064
 QY 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 300
 DB 3065 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 3124
 QY 301 AAGTAGTTCGCCAGTTAATAGTTGGCAACGTTGTCATGTCGCAAGGCAATCGTGGT 360
 DB 3125 AAGTAGTTCGCCAGTTAATAGTTGGCAACGTTGTCATGTCGCAAGGCAATCGTGGT 3184
 QY 361 GTCACGCTCGCTGTTGGTATGCTTCATTCAGTCCGGTTCCTCAAGGAGGAGT 420
 DB 3185 GTCACGCTCGCTGTTGGTATGCTTCATTCAGTCCGGTTCCTCAAGGAGGAGT 3244
 QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTTGT 480
 DB 3245 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTTGT 3304
 QY 481 CAGAAGTAAGTTGGCGCGAG 500
 DB 3305 CAGAAGTAAGTTGGCGCGAG 3324

RESULT 14
 US-09-813-718-5/c
 ; Sequence 5, Application US/09813718
 ; Publication No. US20020182666A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schimmel, Paul
 ; APPLICANT: Wakasugi, Keisuke
 ; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
 ; FILE REFERENCE: 00-221
 ; CURRENT APPLICATION NUMBER: US/09/813,718
 ; CURRENT FILING DATE: 2001-03-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5
 ; LENGTH: 4100
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (3428)..(3961)
 ; OTHER INFORMATION: Description of Artificial Sequence: human TyrRS
 ; OTHER INFORMATION: carboxyl-terminal domain in pBT20B
 US-09-813-718-5
 Query Match 92.4%; Score 462; DB 9; Length 4100;
 Best Local Similarity 99.2%; Pred. No. 3.5e-149;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
 QY 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGGAGGACCTACTCTCA 60
 DB 1485 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGGAGGACCTACTCTCA 1426
 QY 61 GCGATCTGTCTATTTCGTTTCATCCCATAGTTGCTGCAACTCCCGCTCGTGTAGATAACT 120
 DB 1425 GCGATCTGTCTATTTCGTTTCAT -CCATAGTTGCTG -ACTCCCGCTCGTGTAGATAACT 1369
 QY 121 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCAAGACCCACG 180
 DB 1368 ACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCG -AGACCCACG 1310
 QY 181 CTCACGGCTCCAGATTATCAGCAATAAACACGAGCCGAGCGGAGCGGAGGAG 240
 DB 1309 CTCACGGCTCCAGATTATCAGCAATAAACACGAGCCGAGCGGAGCGGAGGAGGAG 1250
 QY 241 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 300
 DB 1249 TGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT 1190
 QY 301 AAGTAGTTCGCCAGTTAATAGTTGGCAACGTTGTCATGTCGCAAGGCAATCGTGGT 360
 DB 1189 AAGTAGTTCGCCAGTTAATAGTTGGCAACGTTGTCATGTCGCAAGGCAATCGTGGT 1130
 QY 361 GTCACGCTCGCTGTTGGTATGCTTCATTCAGTCCGGTTCCTCAAGGAGGAGT 420
 DB 1129 GTCACGCTCGCTGTTGGTATGCTTCATTCAGTCCGGTTCCTCAAGGAGGAGGAGT 1070
 QY 421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTTGT 480
 DB 1069 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTTGT 1010
 QY 481 CAGAAGTAAGTTGGCGCGAG 500
 DB 1009 CAGAAGTAAGTTGGCGCGAG 990

RESULT 15
 US-10-240-532-5/c
 ; Sequence 5, Application US/10240532
 ; Publication No. US20040009163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schimmel, Paul
 ; APPLICANT: Wakasugi, Keisuke
 ; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
 ; FILE REFERENCE: TSRI 720.1
 ; CURRENT APPLICATION NUMBER: US/10/240,532
 ; CURRENT FILING DATE: 2002-09-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/08975
 ; PRIOR APPLICATION NUMBER: 2001-03-21
 ; PRIOR APPLICATION NUMBER: US 60/193,471
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 4100
 ; TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: CDS

LOCATION: (3428)..(3961)

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: human TyrRS

OTHER INFORMATION: carboxyl-terminal domain in pET20B

US-10-240-532-5

Query Match 92.4%; Score 462; DB 17; Length 4100;
 Best Local Similarity 99.2%; Pred. No. 3.5e-149;
 Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

QY 1 ATATATGAGTAAACTTGGCTGACAGTTACCAATGCTTAATCACTGAGGACCTATCTCA 60
 DB 1485 ATATATGAGTAAACTTGGCTGACAGTTACCAATGCTTAATCACTGAGGACCTATCTCA 1426

QY 61 GCGATCTGCTTATTCGTTTCATCCCATAGTTGCCTGCAACTCCCCGTCGTGTAGATAACT 120
 DB 1425 GCGATCTGCTTATTCGTTTCAT-CCATAGTTGCCTG--ACTCCCGTCGTGTAGATAACT 1369

QY 121 ACGATACGGAGGCTTACCATCTGCCCCAGTCTGCTCAATGATACCGCGAAGACCCACG 180
 DB 1368 ACGATACGGAGGCTTACCATCTGCCCCAGTCTGCTCAATGATACCGCG-AGACCCACG 1310

QY 181 CTCACCGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCCCGGCGCAGAG 240
 DB 1309 CTCACCGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGCCCGGCGCAGAG 1250

QY 241 TGGTCTGCAACTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAGCTAGAGT 300
 DB 1249 TGGTCTGCAACTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAGCTAGAGT 1190

QY 301 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTGCCATTGCTGCGGCATCGTGT 360
 DB 1189 AAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTGCCATTGCTGCGGCATCGTGT 1130

QY 361 GTCACGCTCGTGTGGTATGGCTTCATTACGCTCCGTTCCCAACGATCAAGGCGAGT 420
 DB 1129 GTCACGCTCGTGTGGTATGGCTTCATTACGCTCCGTTCCCAACGATCAAGGCGAGT 1070

QY 421 TACATGATCCCATGTTGTGCAAAAAGCGGTAGTCTCTTCGTTCCCTCCGATCGTTGT 480
 DB 1069 TACATGATCCCATGTTGTGCAAAAAGCGGTAGTCTCTTCGTTCCCTCCGATCGTTGT 1010

QY 481 CAGAAGTAAGTTGCCGCGAG 500
 DB 1009 CAGAAGTAAGTTGCCGCGAG 990

Search completed: April 29, 2005, 06:00:46
 Job time : 2580 secs